

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 17:56:17 ; Search time 165 seconds
(without alignments)
147.672 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

Sequence: 1 RSRRATEVTPVPTVTDYD.....AGGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	63	5	Abb76407 Osteopontin
2	236	70.9	87	5	Aae18619 Biosynthe
3	207	62.2	40	5	Abb76406 Osteopontin
4	201	60.4	40	5	Abb76410 Osteopontin
5	200	60.1	40	5	Abb76404 Osteopontin
6	200	60.1	40	5	Abb76411 Osteopontin
7	181	54.4	49	5	Abb76405 Osteopontin
8	181	54.4	192	5	Abg79674 Tumour in
9	181	54.4	218	8	Adsl2215 Human the
10	181	54.4	243	8	Adj67551 Human ova
11	181	54.4	243	8	Adj67676 Human cel
12	181	54.4	273	7	Aao30815 Human ova
13	181	54.4	278	7	Adm47287 Osteopontin
14	181	54.4	279	8	Adsl0984 Human the
15	181	54.4	282	2	Aar30701 Isoform o
16	181	54.4	286	6	Abp58125 Human ost
17	181	54.4	287	4	Aab30575 A human ova
18	181	54.4	287	5	Abg96388 Human ova
19	181	54.4	287	6	Abra7551 Breast ca
20	181	54.4	287	6	Abra92133 Human cer
21	181	54.4	287	7	Adb75483 Prostate
22	181	54.4	287	8	Adq88475 Human OPN
23	181	54.4	290	7	Adm47215 Osteopoti
24	181	54.4	296	2	Aar30700 Human uro
25	181	54.4	299	6	Abp58124 Human ost

ALIGNMENTS

RESULT 1

ABB76407
ID ABB76407 standard; protein; 63 AA.

XX AC

XX ABB76407;

XX 27-AUG-2002 (first entry)

XX Osteopontin-derived peptide.

XX Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;

XX cell differentiation.

XX Homo sapiens.

XX WO200232940-A2.

XX 25-APR-2002.

XX 18-OCT-2001; 2001WO-US032457.

XX 18-OCT-2000; 2000US-0241248P.

XX 05-OCT-2001; 2001US-0327273P.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Askar S, Salcedo J;

XX WPI; 2002-479661/51.

XX Osteopontin derived peptides useful in implants e.g. dental screws or fixtures, and orthopedic joints.

XX Claim 1; Page 8; 64pp; English.

XX The present sequence is an osteopontin-derived peptide, which regulates cell development and binds to an integrin on a cell surface. The invention provides an osteopontin containing implant which increases the rate of osseointegration and the percentage of bone apposition. The implant includes osteopontin, an active fragment of osteopontin or an osteopontin-derived peptide such as the present claimed peptide. Claimed osteopontin derived peptides of the invention (see ABB76403-11) bind to various cell types and play important roles in cellular differentiation and/or motility. These cells include osteoprogenitor cells, tumour cells, macrophages, peritoneal cells, endothelial cells, epithelial cells, eosinophils, stem cells, limited potential precursor cells, precursor cells, committed precursor cells, and differentiated cells. The peptides are also active as antiinflammatory agents. Antibodies provide a

CC mechanism to abolish or attenuate the activities of the claimed peptides.
CC The implant can be used in an osteopontin containing cell recruitment
CC system, to induce new tissue formation in a subject, and to promote cell
CC differentiation (all claimed). The implants include surgical implants
CC such as dental screws or fixtures, jaw modification implants, face
CC reconstitution implants, orthopaedic implants e.g. orthopaedic screws,
CC rods or joints such as hip or knee replacement implants
XX

SQ Sequence 63 AA;

Query Match 100.0%; Score 333; DB 5; Length 63;
Best Local Similarity 100.0%; Pred. No. 6.1e-30;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRATEVTPVPTVDTYDGRGDSVYVGRRSKSKFRRPAGAGGPAGPAGPAGPA 60
Db 1 RRRATEVTPVPTVDTYDGRGDSVYVGRRSKSKFRRPAGAGGPAGPAGPAGPA 60
QY 61 GPA 63
Db 61 GPA 63

RESULT 2
AAE18619
ID AAE18619 standard; protein; 87 AA.
AC AAE18619;

XX 17-MAY-2002 (first entry)

XX Biosynthetic oncolytic molecule, oncolysin 2.

XX Biosynthetic oncolytic molecule; functional domain; osteopontin;
KW cellular apoptosis; apoptotic response; cancer; inflammatory condition;
KW arthritis; integrin receptor; CD44 receptor; cell growth; gene therapy;
KW cytostatic; antiinflammatory; antiarthritic; oncolysin 2.
XX

OS Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..16
FT /label= Signal_peptide
FT Region 17..21
FT /notes= "linker region"
FT Region 22..35
FT /notes= "Golgi processing region"
FT Region 36..40
FT /notes= "liner region"
FT Domain 41..64
FT /label= Apoptotic_domain
FT Domain 62..71
FT /label= Heparin_binding_domain
FT Domain 65..87
FT /label= Collagen_binding_domain

XX WO200196395-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-US019239.

XX 13-JUN-2000; 2000US-0211436P.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Ashkar S, Hikita S, Dehnl G;

XX WPI; 2002-179509/23.

XX Novel biosynthetic oncolytic molecule useful for treating cancer and
PT inflammatory conditions arthritis, comprises apoptotic component and
PT biomodular component, to form a molecule which promotes apoptosis.

XX Claim 30; Fig 2A; 48pp; English.

XX The invention relates to biosynthetic oncolytic molecules which include
CC functional domains derived from osteopontin. These molecules are capable
CC of promoting cellular apoptosis. Biosynthetic oncolytic molecules are
CC useful for modulating an apoptotic response in a cell. These molecules
CC are useful for treating cancer, inflammatory conditions such as
CC arthritis, for elimination of abnormal or unwanted cells that express at
CC least an integrin receptor and/or that co-express both an integrin and a
CC CD44 receptor and for regulating cell growth processes. DNA encoding this
CC molecule is useful in gene therapy. The present sequence is a
CC biosynthetic oncolytic molecule, oncolysin 2

XX Sequence 87 AA;

Query Match 70.9%; Score 236; DB 5; Length 87;
Best Local Similarity 86.8%; Pred. No. 7e-19;
Matches 46; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 10 TPVPTVDTYDGRGDSVYVGRRSKSKFRRPAGAGGPAGPAGPAGPAGP 62
Db 41 TPVPTVDTYDGRGDSVYVGLRSK-----PAGAGGPAGPAGPAGPAGP 87

RESULT 3
ABB76406
ID ABB76406 standard; protein; 40 AA.

XX ABB76406;

XX 27-AUG-2002 (first entry)

XX Osteopontin-derived peptide.

XX Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
KW cell differentiation.

XX Homo sapiens.

XX WO200232940-A2.

XX 25-APR-2002.

XX 18-OCT-2001; 2001WO-US032457.

XX 18-OCT-2000; 2000US-0241248P.

XX 05-OCT-2001; 2001US-0327273P.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Askar S, Salcedo J;

XX WPI; 2002-479661/51.

XX Osteopontin derived peptides useful in implants e.g. dental screws or
PT fixtures, and orthopedic joints.
XX Claim 1; Page 8; 64pp; English.

XX The present sequence is an osteopontin-derived peptide, which regulates
CC cell development and binds to an integrin on a cell surface. The
CC invention provides an osteopontin containing implant which increases the
CC rate of osseointegration and the percentage of bone apposition. The
CC implant includes osteopontin, an active fragment of osteopontin or an
CC osteopontin-derived peptide such as the present claimed peptide. Claimed
CC osteopontin derived peptides of the invention (see ABB76403-11) bind to
CC various cell types and play important roles in cellular differentiation
CC and/or motility. These cells include osteoprogenitor cells, tumour cells,
CC macrophages, stem cells, limited potential precursor cells, epithelial cells,
CC eosinophiles, perosteal cells, endothelial cells, epithelial cells,
CC cells, committed precursor cells, and differentiated cells. The peptides
CC are also active as antiinflammatory agents. Antibodies provide a

CC mechanism to abolish or attenuate the activities of the claimed peptides.
 CC The implant can be used in an osteopontin containing cell recruitment
 CC system, to induce new tissue formation in a subject, and to promote cell
 CC differentiation (all claimed). The implants include surgical implants
 CC such as dental screws or fixtures, jaw modification implants, face
 CC reconstitution implants, orthopaedic implants e.g. orthopaedic screws,
 CC rods or joints such as hip or knee replacement implants
 XX
 SQ Sequence 40 AA;

Query Match 62.2%; Score 207; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.6e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSRRAETEVPVPTVDTYDGRGDSVVGRRSKSKFRFP 40
 |||||
 DB 1 RSRRAETEVPVPTVDTYDGRGDSVVGRRSKSKFRFP 40

RESULT 4
 ABB76410
 ID ABB76410 standard; protein; 40 AA.
 XX
 AC ABB76410;

DT 27-AUG-2002 (first entry)

DE Osteopontin-derived peptide.

KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 cell differentiation.

OS Homo sapiens.

PN WO200232940-A2.

PD 25-APR-2002.

PF 18-OCT-2001; 2001WO-US032457.

PR 18-OCT-2000; 2000US-0241248P.

PS 05-OCT-2001; 2001US-0327273P.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Askar S, Salcedo J;

XX WPI; 2002-479661/51.

XX Osteopontin derived peptides useful in implants e.g. dental screws or
 XX fixtures, and orthopedic joints.

XX Claim 1; Page 8; 64pp; English.

XX The present sequence is an osteopontin-derived peptide, which regulates
 CC cell development and binds to an integrin on a cell surface. The
 CC invention provides an osteopontin containing implant which increases the
 CC rate of osseointegration and the percentage of bone apposition. The
 CC implant includes osteopontin, an active fragment of osteopontin or an
 CC osteopontin-derived peptide such as the present claimed peptide. Claimed
 CC osteopontin-derived peptides of the invention (see ABB76403-11) bind to
 CC various cell types and play important roles in cellular differentiation
 CC and/or motility. These cells include osteoprogenitor cells, tumour cells,
 CC macrophages, peritoneal cells, endothelial cells, epithelial cells,
 CC eosinophils, stem cells, limited potential precursor cells, precursor
 CC cells, committed precursor cells, and differentiated cells. The peptides
 CC are also active as antiinflammatory agents. Antibodies provide a
 CC mechanism to abolish or attenuate the activities of the claimed peptides.
 CC The implant can be used in an osteopontin containing cell recruitment
 CC system, to induce new tissue formation in a subject, and to promote cell
 CC differentiation (all claimed). The implants include surgical implants
 CC such as dental screws or fixtures, jaw modification implants, face
 CC reconstitution implants, orthopaedic implants e.g. orthopaedic screws,

CC rods or joints such as hip or knee replacement implants
 XX
 SQ Sequence 40 AA;

Query Match 60.4%; Score 201; DB 5; Length 40;
 Best Local Similarity 97.5%; Pred. No. 2.6e-15;
 Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSRRAETEVPVPTVDTYDGRGDSVVGRRSKSKFRFP 40
 |||||
 DB 1 RSRRAETEVPVPTVDTYDGRGDSVVGRRSKSKFRFP 40

RESULT 5
 ABB76404
 ID ABB76404 standard; protein; 40 AA.
 XX
 AC ABB76404;

DT 27-AUG-2002 (first entry)

DE Osteopontin-derived peptide OC-1016.

KW Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;
 cell differentiation.

OS Homo sapiens.

PN WO200232940-A2.

PD 25-APR-2002.

PF 18-OCT-2001; 2001WO-US032457.

PR 18-OCT-2000; 2000US-0241248P.

PS 05-OCT-2001; 2001US-0327273P.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Askar S, Salcedo J;

XX WPI; 2002-479661/51.

XX Osteopontin derived peptides useful in implants e.g. dental screws or
 XX fixtures, and orthopedic joints.

XX Claim 1; Page 59; 64pp; English.

XX The present sequence is osteopontin-derived peptide OC-1016, which
 CC regulates cell development and binds to an integrin on a cell surface.
 CC The invention provides an osteopontin containing implant which increases
 CC the rate of osseointegration and the percentage of bone apposition. The
 CC implant includes osteopontin, an active fragment of osteopontin or an
 CC osteopontin-derived peptide such as the present, preferred peptide.
 CC Claimed osteopontin derived peptides of the invention (see ABB76403-11)
 CC bind to various cell types and play important roles in cellular
 CC differentiation and/or motility. These cells include osteoprogenitor
 CC cells, tumour cells, macrophages, periosteal cells, endothelial cells,
 CC epithelial cells, eosinophils, stem cells, limited potential precursor
 CC cells, precursor cells, committed precursor cells, and differentiated
 CC cells. The peptides are also active as antiinflammatory agents.
 CC Antibodies provide a mechanism to abolish or attenuate the activities of
 CC the claimed peptides. The implant can be used in an osteopontin
 CC containing cell recruitment system, to induce new tissue formation in a
 CC subject, and to promote cell differentiation (all claimed). The implants
 CC include surgical implants such as dental screws or fixtures, jaw
 CC modification implants, face reconstitution implants, orthopaedic implants
 CC e.g. orthopaedic screws, rods or joints such as hip or knee replacement
 CC implants

XX Sequence 40 AA;

Query Match 60.1%; Score 200; DB 5; Length 40;

Best Local Similarity 97.5%; Pred. No. 3.4e-15;		Matches 39; Conservative 0; Mismatches 0; Gaps 0;	
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1 RSRRATEVFTPVVPTVDTYDGRGDSVVYGRRSKSKKFRFP 40 		
Db	1 RSRRATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRFP 40 		
RESULT 6			
ABB76411			
ID	ABB76411 standard; protein; 40 AA.		
XX			
AC	ABB76411;		
XX			
DT	27-AUG-2002 (first entry)		
XX			
DE	Osteopontin-derived peptide moc-1016.		
XX			
KW	Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;		
KW	cell differentiation.		
XX			
OS	Homo sapiens.		
XX			
FN	WO200232940-A2.		
XX			
PD	25-APR-2002.		
XX			
PF	18-OCT-2001; 2001WO-US032457.		
XX			
PR	18-OCT-2000; 2000US-0241248P.		
XX			
XX	05-OCT-2001; 2001US-0327273P.		
XX			
PA	(CHIL-) CHILDRENS MEDICAL CENT.		
XX			
PI	Askar S, Salcedo J;		
XX			
DR	WPI; 2002-479661/51.		
XX			
PT	Osteopontin derived peptides useful in implants e.g. dental screws or		
PT	fixtures, and orthopedic joints.		
XX			
PS	Claim 1; Page 59; 64pp; English.		
XX			
CC	The present sequence is osteopontin-derived peptide moc-1016, which		
CC	regulates cell development and binds to an integrin on a cell surface.		
CC	The invention provides an osteopontin containing implant which increases		
CC	the rate of osseointegration and the percentage of bone apposition. The		
CC	implant includes osteopontin, an active fragment of osteopontin or an		
CC	osteopontin-derived peptide such as the present, preferred peptide.		
CC	Claimed osteopontin derived peptides of the invention (see ABB76403-11)		
CC	bind to various cell types and play important roles in cellular		
CC	differentiation and/or motility. These cells include osteoprogenitor		
CC	cells, tumour cells, macrophages, periosteal cells, endothelial cells,		
CC	epithelial cells, eosinophils, stem cells, limited potential precursor		
CC	cells, precursor cells, committed precursor cells, and differentiated		
CC	cells. The peptides are also active as antiinflammatory agents.		
CC	Antibodies provide a mechanism to abolish or attenuate the activities of		
CC	the claimed peptides. The implant can be used in an osteopontin		
CC	containing cell recruitment system, to induce new tissue formation in a		
CC	subject, and to promote cell differentiation (all claimed). The implants		
CC	include surgical implants such as dental screws or fixtures, jaw		
CC	modification implants, face reconstitution implants, orthopaedic implants		
CC	e.g. orthopaedic screws, rods or joints such as hip or knee replacement		
CC	implants		
XX			
SQ	Sequence 40 AA;		
Query Match 60.1%; Score 200; DB 5; Length 40;			
Best Local Similarity 97.5%; Pred. No. 3.4e-15;			
		Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	5 ATEVFTPVVPTVDTYDGRGDSVVYGRRSKSKKFRFP 40 		
Db	14 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRFP 49 		

Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		Matches 39; Conservative 0; Mismatches 0; Gaps 0;	
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1 RSRRATEVFTPVVPTVDTYDGRGDSVVYGRRSKSKKFRFP 40 		
Db	1 RSRRATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRFP 40 		
RESULT 7			
ABB76405			
ID	ABB76405 standard; protein; 49 AA.		
XX			
AC	ABB76405;		
XX			
DT	27-AUG-2002 (first entry)		
XX			
DE	Osteopontin-derived peptide.		
XX			
KW	Osteopontin; osteopathic; bone; tissue formation; antiinflammatory;		
KW	cell differentiation.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200232940-A2.		
XX			
PD	25-APR-2002.		
XX			
PF	18-OCT-2001; 2001WO-US032457.		
XX			
PR	18-OCT-2000; 2000US-0241248P.		
XX			
PR	05-OCT-2001; 2001US-0327273P.		
XX			
XX	(CHIL-) CHILDRENS MEDICAL CENT.		
XX			
PI	Askar S, Salcedo J;		
XX			
XX	WPI; 2002-479661/51.		
XX			
PT	Osteopontin derived peptides useful in implants e.g. dental screws or		
PT	fixtures, and orthopedic joints.		
XX			
PS	Claim 1; Page 8; 64pp; English.		
XX			
CC	The present sequence is an osteopontin-derived peptide, which regulates		
CC	cell development and binds to an integrin on a cell surface. The		
CC	invention provides an osteopontin containing implant which increases the		
CC	rate of osseointegration and the percentage of bone apposition. The		
CC	implant includes osteopontin, an active fragment of osteopontin or an		
CC	osteopontin-derived peptide such as the present claimed peptide. Claimed		
CC	osteopontin derived peptides of the invention (see ABB76403-11) bind to		
CC	various cell types and play important roles in cellular differentiation		
CC	and/or motility. These cells include osteoprogenitor cells, tumour cells,		
CC	macrophages, periosteal cells, endothelial cells, epithelial cells,		
CC	eosinophils, stem cells, limited potential precursor cells, precursor		
CC	cells, committed precursor cells, and differentiated cells. The peptides		
CC	are also active as antiinflammatory agents. Antibodies provide a		
CC	mechanism to abolish or attenuate the activities of the claimed peptides.		
CC	The implant can be used in an osteopontin containing cell recruitment		
CC	system, to induce new tissue formation in a subject, and to promote cell		
CC	differentiation (all claimed). The implants include surgical implants		
CC	such as dental screws or fixtures, jaw modification implants, face		
CC	reconstitution implants, orthopaedic implants e.g. orthopaedic screws,		
CC	rods or joints such as hip or knee replacement implants		
XX			
SQ	Sequence 49 AA;		
Query Match 54.4%; Score 181; DB 5; Length 49;			
Best Local Similarity 97.2%; Pred. No. 5.8e-13;			
		Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	5 ATEVFTPVVPTVDTYDGRGDSVVYGRRSKSKKFRFP 40 		
Db	14 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRFP 49 		

RESULT 8
ABG79674
ID ABG79674 standard; protein; 192 AA.
XX AC
XX ABG79674;
DT 15-NOV-2002 (first entry)
DE Tumour involved gene (TIG) splice variant protein, NV-5.
XX Human; splice variant; tumour-involved gene; TIG;
KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
KW endothelial cell; cell differentiation; cell proliferation; apoptosis;
XX gene therapy.
XX Homo sapiens.
OS
XX US2002086384-A1.
XX 04-JUL-2002.
XX
XX 13-MAR-2001; 2001US-00805020.
XX 14-MAR-2000; 2000IL-00135402.
XX 16-MAY-2000; 2000IL-00136154.
XX (LEVI/) LEVINE Z.
XX (DAVI/) DAVID A.
XX (ROMA/) ROMANO C.
XX (BERN/) BERNSTEIN J.
XX
XX Levine Z, David A, Romano C, Bernstein J;
XX WPI; 2002-635679/68.
XX N-PSDB; ABS65204.
XX
XX Novel nucleic acid sequence, which is an alternative splicing variant of
XX tumor involved genes, useful for detecting cancer, predisposition to
XX cancer, for evaluating cancer state and in gene therapy for treating
XX cancer.
XX
XX Claim 4; Page 70-71; 180pp; English.
XX
XX The invention discloses isolated human nucleic acid alternative splicing
XX variants that are all tumour-involved genes (TIGs). The nucleic acid and
XX polypeptides are useful for determining the level of a nucleic acid or
XX polypeptide in a biological sample, for detecting a variant nucleic acid
XX or polypeptide sequence in a biological sample, for determining the level
XX of variant nucleic acid or polypeptide sequences in a biological sample
XX and for determining the ratio between the level of variant sequence in a
XX first biological sample and the level of the original sequence from which
XX the variant has been varied by alternative splicing in a second
XX biological sample and for raising antibodies. A pharmaceutical
XX composition comprising a carrier and the nucleic acid, is useful for
XX treating diseases (e.g. cancer) that can be ameliorated or cured by
XX increasing or decreasing the level of the encoded protein. The nucleic
XX acids are also useful for diagnostic purposes, especially for detecting
XX cancer or a predisposition to cancer, for evaluating the state or
XX aggressiveness of cancer disease, in basic research, for understanding
XX the physiological function of the original TIG, in targeting or
XX developing pharmaceuticals, for distinguishing various stages in the life
XX cycle of the same type of cells which may be helpful for the development
XX of pharmaceuticals for various cancer stages in which cell cycle is non-
XX normal, for determining mutations in tumour-involved genes and in gene
XX therapy. The polypeptides are useful for identifying compounds capable of
XX binding to the variant product and modulating its activity and for
XX modulating endothelial differentiation and proliferation, as well as to
XX modulate apoptosis either ex vivo or in vivo. The sequences presented in
XX ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
XX disclosed
XX
XX Sequence 192 AA;

Query Match 54.4%; Score 181; DB 5; Length 192;
Best Local Similarity 97.2%; Pred. No. 2.5e-12;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ATEVTPVPVPTVDYDGRGDSVVYGRRSKSKKFRFP 40
DB 142 ATEVTPVPVPTVDYDGRGDSVVYGLRSKSKKFRFP 177
|||||
RESULT 9
ADS12215
ID ADS12215 standard; protein; 218 AA.
XX AC
XX ADS12215;
XX 16-DEC-2004 (first entry)
XX Human therapeutic contig protein - SEQ ID 2452.
XX
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT Misc-difference 1..218 /label= Unknown, OTHER
FT /note= "OTHER = In-frame STOP codon"
XX
XX WO2004080148-A2.
XX
XX 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI; 2004-668857/65.
XX N-PSDB; ADS11617.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.
XX
XX Example 2; SEQ ID NO 2452; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX disorders, such as aplastic anaemia or cancer, as well as for promoting
XX wound healing. The molecules may also be utilised during gene therapy
XX procedures. The current sequence is that of a human therapeutic contig
XX protein of the invention.
XX
XX Sequence 218 AA;
QY 5 ATEVTPVPVPTVDYDGRGDSVVYGRRSKSKKFRFP 40
DB 169 ATEVTPVPVPTVDYDGRGDSVVYGLRSKSKKFRFP 204
|||||

[illegible]

PI Baughn MR, Becha SD, Bhatia U, Blake JU, Borowsky ML, Burrill JD;
 PI Deleage AM, Elliott VS, Gandhi AR, Gietzen KJ, Gorvad AE;
 PI Griffin JA, Ho A, Jin P, Kable AE, Lal PG, Lee S, Lee SY;
 PI Marquis JP, Lehr-Mason FM, Ramkumar J, Richardson TW, Sprague WW;
 PI Swarnakar A, Tang TY, Tran B, Tran UK, Chawia NK, Warren BA, Xu Y;
 XX Yue H, Zheng W;
 DR WPI; 2003-513695/48.
 DR N-PSDB; AAL62017.
 XX
 PT New human cell adhesion and extracellular matrix proteins (CADECM)
 PT polypeptide, useful for preparing a composition for treating a disease
 PT associated with decreased expression or overexpression of CADECM e.g.,
 PT cancer.
 XX
 PS Claim 1; Page 277; 374pp; English.
 XX
 CC The invention relates to human cell adhesion and extracellular matrix
 CC proteins (CADECM) and nucleic acid molecules encoding such proteins.
 CC CADECM proteins are useful for preparing a composition for diagnosing or
 CC treating a disease or condition associated with decreased expression or
 CC overexpression of functional CADECM e.g., immune disorders or cancer. The
 CC invention is also useful in gene therapy. The present sequence is human
 CC CADECM protein
 XX
 SQ Sequence 273 AA;

Query Match 54.4%; Score 181; DB 7; Length 273;
 Best Local Similarity 97.2%; Pred. No. 3.6e-12;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKFRPP 40
 DB 101 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKFRPP 136

RESULT 13

ADM47287

ID ADM47287 standard; protein; 278 AA.

AC ADM47287;

DT 03-JUN-2004 (first entry)

DE Osteopontin like NOVX 11b protein.

XX NOVX; cytostatic; gene therapy; vaccine; cancer; chromosome mapping.

XX Unidentified.

XX WO2003083039-A2.

XX 09-OCT-2003.

XX 03-JUL-2002; 2002WO-US021485.

XX 05-JUL-2001; 2001US-0303046P.

XX 09-JUL-2001; 2001US-0303828P.

XX 11-JUL-2001; 2001US-0304502P.

XX 12-JUL-2001; 2001US-0305011P.

XX 13-JUL-2001; 2001US-0305262P.

XX 16-JUL-2001; 2001US-0305673P.

XX 17-JUL-2001; 2001US-0306085P.

XX 24-JUL-2001; 2001US-0307536P.

XX 27-JUL-2001; 2001US-0308228P.

XX 30-JUL-2001; 2001US-0308677P.

XX 14-AUG-2001; 2001US-0312203P.

XX 17-SEP-2001; 2001US-0322640P.

XX 19-SEP-2001; 2001US-0323484P.

XX 21-SEP-2001; 2001US-0323821P.

XX 21-SEP-2001; 2001US-0323948P.

XX 25-SEP-2001; 2001US-0324711P.

XX 09-OCT-2001; 2001US-0327893P.

PR 21-NOV-2001; 2001US-0331768P.
 PR 21-FEB-2002; 2002US-0359191P.
 PR 22-FEB-2002; 2002US-035939P.
 PR 28-FEB-2002; 2002US-0360923P.
 PR 01-MAR-2002; 2002US-0360830P.
 PR 01-MAR-2002; 2002US-0361178P.
 PR 05-MAR-2002; 2002US-0361748P.
 PR 12-MAR-2002; 2002US-0363429P.
 PR 12-MAR-2002; 2002US-0363683P.
 PR 12-MAR-2002; 2002US-0372141P.
 PR 16-APR-2002; 2002US-0372967P.
 PR 16-APR-2002; 2002US-0373051P.
 PR 16-APR-2002; 2002US-0373063P.
 PR 17-APR-2002; 2002US-0373280P.
 PR 17-APR-2002; 2002US-0373287P.
 PR 19-APR-2002; 2002US-0373881P.
 PR 02-JUL-2002; 2002US-00187975.
 XX
 XX (CURA-) CURAGEN CORP.

XX Li L, Shenoy SG, Patturajan M, Ellerman K, Gorman L, Zhong M;
 PI Catterton E, Spytek KA, Miller CE, Edinger SR, Hjalit T, Gerlach VL;
 PI Shinkets RA, Taupier RJ, Anderson DW, Guo X, Baumgartner JC;
 PI Padigaru M, Peyman JA, Smithson G, Casman SJ, Voss EZ, Boldog FL;
 PI Pena CEA, Chapoval A, Rastelli L, Kekuda R, Vernet CM;
 XX
 DR WPI; 2003-812538/76.
 DR N-PSDB; ADM47286.

XX New NOVX polypeptide, useful for preparing a composition for treating or
 preventing e.g. cancer or for chromosome mapping.
 PT
 PT Claim 2; SEQ ID NO 120; 433pp; English.
 PS
 XX The invention relates to a novel isolated polypeptide, designated NOVX.
 CC The novel polypeptide comprises a sequence comprising 109-1671 amino
 CC acids, or its mature form; a sequence that is at least 95% identical to
 CC the 109-1671 amino acid polypeptide; or a sequence comprising one or more
 CC conservative substitutions in the 109-1671 amino acid polypeptide. The
 CC invention further comprises: a composition; a kit comprising the
 CC polypeptide; a method for determining the presence or amount of the
 CC polypeptide or nucleic acid molecule in a sample; determining the
 CC presence of, or predisposition to, a disease associated with the altered
 CC levels of nucleic acid or of expression of the polypeptide in a first
 CC mammalian subject; identification of an agent that binds to the
 CC polypeptide; identification of a potential therapeutic agent for treating
 CC a pathology related to aberrant expression or physiological interactions
 CC of the polypeptide; a method of screening for a modulator of activity or
 CC latency of, or predisposition to, a pathology associated with the
 CC polypeptide; a method for modulating the activity of the polypeptide;
 CC treating or preventing a pathology associated with the polypeptide;
 CC treating a pathological state in a mammal; an isolated nucleic acid
 CC molecule; a vector comprising the nucleic acid molecule; a cell
 CC comprising the vector; an antibody that immunospecifically binds to the
 CC polypeptide; and a method for producing the polypeptide. The NOVX
 CC polypeptide and its encoding nucleic acid have cytostatic activity. The
 CC NOVX polynucleotide can be used in gene therapy to treat disorders. The
 CC NOVX polypeptide can be used to create a vaccine. The polypeptide is
 CC useful for preparing a composition for treating or preventing a
 CC pathological state in a mammal, e.g., cancer, or for chromosome mapping.
 CC This sequence represents a NOVX polypeptide of the invention.

XX Sequence 278 AA;

Query Match 54.4%; Score 181; DB 7; Length 278;
 Best Local Similarity 97.2%; Pred. No. 3.7e-12;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKFRPP 40
 DB 128 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKFRPP 163

```

RESULT 14
ADSI0984
ID ADSI0984 standard; protein; 279 AA.
XX
XX
AC ADSI0984;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human therapeutic protein - SEQ ID 1221.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopolesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2004080148-A2.
XX
PD 23-SEP-2004.
XX
PF 30-SEP-2003; 2003WO-US030720.
XX
PR 02-OCT-2002; 2002US-0416186P.
XX
PA (NUVE-) NUVELO INC.
XX
PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX
XX WPI: 2004-668857/65.
DR N-PSDB; ADSI0300.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
XX Claim 20; SEQ ID NO 1221; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
XX
SQ Sequence 279 AA;
Query Match 54.4%; Score 181; DB 8; Length 279;
Best Local Similarity 97.2%; Pred. No. 3.7e-12;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRFP 40
Db 115 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRFP 150

RESULT 15
AAR30701
ID AAR30701 standard; protein; 282 AA.
XX
XX
AC AAR30701;
XX
DT 25-MAR-2003 (revised)
DT 14-MAY-1993 (first entry)
XX
XX Isoform of human osteopontin protein.
DE Human; HUP; osteopontin; kidney stone; osteoporosis.
XX
XX
OS Homo sapiens.
XX
PN WO9222316-A1.
XX
PD 23-DEC-1992.
XX
PF 01-JUN-1992; 92WO-US004599.
XX
PR 10-JUN-1991; 91US-00712476.
XX
XX (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX (UYPE-) UNIV PENNSYLVANIA.
XX (UYCA-) UNIV CAMBRIDGE.
XX
PI Hoyer J, Neilson E, Sinclair J, Clayman M, Shiraga H;
PI Borysiewicz L;
XX
XX WPI: 1993-017903/02.
XX
XX Compn. for treating kidney stone diseases, osteoporosis, etc. - contains
PT aspartic acid-rich protein, and proteins having homology of active
PT portions.
XX
XX Disclosure; Page 41; 65pp; English.
XX
XX To protein is an isoform of human osteopontin (see Young, et al.,
CC Genomics, Vol. 7, pp. 491-502, 1990). The last 4 amino acids of the HUP
CC sequences are deleted from the isoform encoded by mRNA from human bone,
CC decidua and kidney. The sequence may be used to design probes and primers
CC for the isolation of HUP DNA. See also AAR30700. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 282 AA;
Query Match 54.4%; Score 181; DB 2; Length 282;
Best Local Similarity 97.2%; Pred. No. 3.7e-12;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRFP 40
Db 110 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRFP 145

Search completed: July 27, 2005, 18:11:55
Job time : 168 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:06:23 ; Search time 42 seconds
(without alignments)
111,974 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

Sequence: 1 RRRATEVTPVPTVTDYD.....ACGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	181	54.4	282	1	US-07-712-476A-5
2	181	54.4	296	1	US-07-712-476A-1
3	181	54.4	300	4	US-09-949-016-5962
4	181	54.4	314	4	US-09-134-253-1
5	181	54.4	314	4	US-09-206-576-2
6	181	54.4	314	4	US-09-538-092-896
7	181	54.4	329	4	US-09-949-016-10363
8	177	53.2	300	6	5340934-6
9	177	53.2	300	6	5340934-6
10	160	48.0	32	4	US-09-134-253-6
11	118	35.4	278	6	5340934-8
12	118	35.4	278	6	5340934-8
13	111	33.3	317	4	US-09-485-077A-17
14	95.5	28.7	1057	3	US-08-931-820-1
15	95.5	28.7	1341	3	US-08-963-825-18
16	95.5	28.7	1341	3	US-09-811-18
17	95.5	28.7	1341	3	US-09-500-811-18
18	95.5	28.7	1341	3	US-09-570-573-18
19	95.5	28.7	1341	3	US-09-548-608-18
20	91.5	27.5	1024	3	US-09-331-347C-21
21	91.5	27.5	1366	3	US-08-963-825-19
22	91.5	27.5	1366	3	US-09-500-811-19
23	91.5	27.5	1366	3	US-09-570-573-19
24	91.5	27.5	1366	3	US-09-548-608-19
25	91.5	27.5	1366	4	US-09-585-887-10
26	91.5	27.5	1366	4	US-09-289-578-10
27	91.5	27.5	1366	4	US-09-949-016-5882

28	91.5	27.5	1461	4	US-09-585-887-9	Sequence 9, Appli
29	91.5	27.5	1461	4	US-09-289-578-9	Sequence 9, Appli
30	91.5	27.5	1516	4	US-09-949-016-8209	Sequence 8209, Ap
31	89	26.7	54	2	US-08-316-650-14	Sequence 14, Appl
32	89	26.7	54	5	PCT-US95-02251-14	Sequence 12731, A
33	89	26.7	435	4	US-09-902-540-12731	Sequence 10, Appl
34	89	26.7	1017	4	US-08-468-996-10	Sequence 3, Appli
35	89	26.7	1060	3	US-08-931-820-3	Sequence 20, Appl
36	89	26.7	1418	3	US-08-963-825-20	Sequence 1, Appli
37	89	26.7	1418	3	US-09-010-999-1	Sequence 20, Appl
38	89	26.7	1418	3	US-09-500-811-20	Sequence 20, Appl
39	89	26.7	1418	3	US-09-570-573-20	Sequence 20, Appl
40	89	26.7	1418	3	US-09-548-608-20	Sequence 12, Appl
41	89	26.7	1442	2	US-08-316-650-12	Sequence 12, Appl
42	89	26.7	1442	5	PCT-US95-02251-12	Sequence 2, Appli
43	87.5	26.3	279	3	US-09-010-999-2	Sequence 11, Appl
44	87.5	26.3	492	4	US-08-468-996-11	Sequence 23, Appl
45	87	26.1	308	3	US-08-956-307B-23	

ALIGNMENTS

RESULT 1
US-07-712-476A-5
; Sequence 5, Application US/07712476A
; Patent No. 5304496
; GENERAL INFORMATION:
; APPLICANT: Hoyer et al.
; TITLE OF INVENTION: Biological Regulation of
; TITLE OF INVENTION: Mineralization
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 5304496ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/712,476A
; FILING DATE: 19910610
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Suzanne E. Miller
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN 0473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568 3100
; TELEFAX: (215) 568 3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-712-476A-5

Query Match 54.4%; Score 181; DB 1; Length 282;

Best Local Similarity 97.2%; Pred. No. 6.5e-13; Indels 0; Gaps 0; Matches 35; Conservative 0; Mismatches 1;

QY 5 ATEVFTPVVPTVTDYDGRGDSVYVGRSKSKKFRFP 40

Db 110 ATEVFTPVVPTVTDYDGRGDSVYVGRSKSKKFRFP 145

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RESULT 2
US-07-712-476A-1
; Sequence 1, Application US/07712476A
; Patent No. 5304496
; GENERAL INFORMATION:
; APPLICANT: Hoyer et al.
; TITLE OF INVENTION: Biological Regulation of
; TITLE OF INVENTION: Mineralization
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5304496ris
; STREET: One Liberty Place
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07712,476A
; FILING DATE: 19910610
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Suzanne E. Miller
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN 0473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568 3100
; TELEFAX: (215) 568 3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-712-476A-1

Query Match 54.4%; Score 181; DB 1; Length 296;
Best Local Similarity 97.2%; Pred. No. 6.9e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
Db 124 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 159

RESULT 3
US-09-949-016-5962
; Sequence 5962, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5962
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5962

Query Match 54.4%; Score 181; DB 4; Length 300;
Best Local Similarity 97.2%; Pred. No. 7e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
Db 128 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 163

RESULT 4
US-09-134-253-1
; Sequence 1, Application US/09134253
; Patent No. 6509026
; GENERAL INFORMATION:
; APPLICANT: Ashkar, Sammy
; TITLE OF INVENTION: Osteopontin Coated Surfaces and Methods of Use
; FILE REFERENCE: cme-100cp
; CURRENT APPLICATION NUMBER: US/09/134,253
; CURRENT FILING DATE: 1998-08-14
; EARLIER APPLICATION NUMBER: 08/916,912
; EARLIER FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-134-253-1

Query Match 54.4%; Score 181; DB 4; Length 314;
Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
Db 142 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 177

RESULT 5
US-09-206-576-2
; Sequence 2, Application US/09206576
; Patent No. 6551990
; GENERAL INFORMATION:
; APPLICANT: Giachelli, Cecilia M.
; APPLICANT: Steitz, Susie
; TITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification
; FILE REFERENCE: P-UW 3244
; CURRENT APPLICATION NUMBER: US/09/206,576
; CURRENT FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-206-576-2

Query Match 54.4%; Score 181; DB 4; Length 314;
Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
Db 142 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 177

RESULT 6
US-09-206-576-2

Query Match 54.4%; Score 181; DB 4; Length 314;
Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRRP 40
Db 142 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 177

RESULT 6
```

```
US-09-538-092-896
; Sequence 896, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 896
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number P10451
; US-09-538-092-896

Query Match      54.4%; Score 181; DB 4; Length 314;
Best Local Similarity 97.2%; Pred. No. 7.3e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRPP 40
|||||:|||||:|||||:|||||:|||||:|||||:
Db 142 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRPP 177

RESULT 7
US-09-949-016-10363
; Sequence 10363, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10363
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10363

Query Match      54.4%; Score 181; DB 4; Length 329;
Best Local Similarity 97.2%; Pred. No. 7.7e-13;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRPP 40
|||||:|||||:|||||:|||||:|||||:|||||
Db 157 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRPP 192

RESULT 8
5340934-6
; Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
```

```
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:6;
; LENGTH: 300
5340934-6

Query Match      53.2%; Score 177; DB 6; Length 300;
Best Local Similarity 94.4%; Pred. No. 2e-12;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRPP 40
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Db 128 ATEVFSPPVPTVDTYDGRGDSVVYGLRSKSKKFRPP 163

RESULT 9
5340934-6
; Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:6;
; LENGTH: 300
5340934-6

Query Match      53.2%; Score 177; DB 6; Length 300;
Best Local Similarity 94.4%; Pred. No. 2e-12;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRPP 40
|||||:|||||:|||||:|||||:|||||:|||||
Db 128 ATEVFSPPVPTVDTYDGRGDSVVYGLRSKSKKFRPP 163

RESULT 10
US-09-134-253-6
; Sequence 6, Application US/09134253
; Patent No. 6509026
; GENERAL INFORMATION:
; APPLICANT: Ashkar, Sammy
; TITLE OF INVENTION: Osteopontin Coated Surfaces and Methods of Use
; FILE REFERENCE: cme-100cp
; CURRENT APPLICATION NUMBER: US/09/134,253
; CURRENT FILING DATE: 1998-08-14
; EARLIER APPLICATION NUMBER: 08/916,912
; EARLIER FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-134-253-6

Query Match      48.0%; Score 160; DB 4; Length 32;
Best Local Similarity 96.9%; Pred. No. 1.4e-11;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 VFTPVVPTVDTYDGRGDSVVYGRSKSKKFR 39
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Db 1 VFTPVVPTVDTYDGRGDSVVYGLRSKSKKFR 32

RESULT 11
5340934-8
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; Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:8:
; LENGTH: 278
5340934-8
Query Match 35.4%; Score 118; DB 6; Length 278;
Best Local Similarity 68.8%; Pred. No. 9.2e-06;
Matches 22; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 8 VFTPVVPTVTDYDGRGDSVYVGRRSKSKKFR 39
138 VFTPIPTESANDGRGDSVAYGLKRSKKFR 169
Db
RESULT 12
5340934-8
; Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
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; LENGTH: 278
5340934-8
Query Match 35.4%; Score 118; DB 6; Length 278;
Best Local Similarity 68.8%; Pred. No. 9.2e-06;
Matches 22; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 8 VFTPVVPTVTDYDGRGDSVYVGRRSKSKKFR 39
138 VFTPIPTESANDGRGDSVAYGLKRSKKFR 169
Db
RESULT 13
US-09-485-077A-17
; Sequence 17, Application US/09485077A
; Patent No. 6458590
; GENERAL INFORMATION:
; APPLICANT: Mukherjee, Anil
; APPLICANT: Kundu, Gopal
; APPLICANT: Panda, Dibyendu
; TITLE OF INVENTION: Methods and Compositions for Treatment of Restenosis
; FILE REFERENCE: NIH-05047
; CURRENT APPLICATION NUMBER: US/09/485,077A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/US98/16569
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: 60/054,967
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Rattus No. 6458590vegicus
US-09-485-077A-17
Query Match 33.3%; Score 111; DB 4; Length 317;
Best Local Similarity 64.5%; Pred. No. 6.6e-05;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 7 EVFTPVVPTVTDYDGRGDSVYVGRRSKSKKFR 37
; Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:8:
; LENGTH: 278
5340934-8
Query Match 35.4%; Score 118; DB 6; Length 278;
Best Local Similarity 68.8%; Pred. No. 9.2e-06;
Matches 22; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 8 VFTPVVPTVTDYDGRGDSVYVGRRSKSKKFR 39
138 VFTPIPTESANDGRGDSVAYGLKRSKKFR 169
Db
RESULT 14
US-08-931-820-1
; Sequence 1, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Assay for collagen degradation
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96202596.1
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1057 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Collagen type I
US-08-931-820-1
Query Match 28.7%; Score 95.5; DB 3; Length 1057;
Best Local Similarity 65.5%; Pred. No. 0.015;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;
QY 40 PAGAG-----GPAGPAGPAGPAGPAGPA 63
898 PAGSGDRGETGPAGPAGPAGPAGPAGPA 926
Db
RESULT 15
US-08-963-825-18
; Sequence 18, Application US/08963825
; Patent No. 6110689
; GENERAL INFORMATION:
; APPLICANT: Oviat, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,825
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; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,319
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1341 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN ALPHA 1 (I)
; US-08-963-825-18

Query Match 28.7%; Score 95.5; DB 3; Length 1341;
Best Local Similarity 65.5%; Pred. No. 0.019; 4; Indels 5; Gaps 1;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

Qy 40 PAGAAG-----GPAGPAGPAGPAGPAGPA 63
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Job time : 46 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:14:59 ; Search time 154 Seconds
(without alignments)
159.133 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

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Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	236	70.9	87	17	US-10-900-512-6
3	181	54.4	192	9	US-09-805-020-41
4	181	54.4	278	15	US-10-187-975-120
5	181	54.4	286	16	US-10-477-876-3
6	181	54.4	287	14	US-10-097-340-231
7	181	54.4	287	14	US-10-171-311-176
8	181	54.4	287	14	US-10-205-823-307
9	181	54.4	287	14	US-10-177-293-340
10	181	54.4	287	14	US-10-301-822-147
11	181	54.4	287	16	US-10-678-355-6
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 41, Appli
					Sequence 120, App
					Sequence 3, Appli
					Sequence 231, App
					Sequence 176, App
					Sequence 307, App
					Sequence 340, App
					Sequence 147, App
					Sequence 6, Appli

12	181	54.4	290	15	US-10-187-975-48	Sequence 48, Appli
13	181	54.4	299	16	US-10-477-876-2	Sequence 2, Appli
14	181	54.4	300	9	US-09-919-770-2	Sequence 229, App
15	181	54.4	300	14	US-10-097-340-229	Sequence 174, App
16	181	54.4	300	14	US-10-171-311-174	Sequence 305, App
17	181	54.4	300	14	US-10-205-823-305	Sequence 338, App
18	181	54.4	300	14	US-10-177-293-338	Sequence 145, App
19	181	54.4	300	14	US-10-301-822-145	Sequence 267, App
20	181	54.4	300	15	US-10-170-385-267	Sequence 508, App
21	181	54.4	300	15	US-10-295-027-508	Sequence 1333, Ap
22	181	54.4	300	15	US-10-295-027-1333	Sequence 12, Appli
23	181	54.4	300	15	US-10-087-080-12	Sequence 15, Appli
24	181	54.4	300	15	US-10-229-345-15	Sequence 15, Appli
25	181	54.4	300	15	US-10-274-177-15	Sequence 4, Appli
26	181	54.4	300	16	US-10-650-112-15	Sequence 15, Appli
27	181	54.4	300	16	US-10-678-355-4	Sequence 8, Appli
28	181	54.4	300	16	US-10-764-649-8	Sequence 75, Appli
29	181	54.4	300	16	US-10-734-564-75	Sequence 31, Appli
30	181	54.4	300	17	US-10-690-880-31	Sequence 22, Appli
31	181	54.4	300	17	US-10-818-066-22	Sequence 42, Appli
32	181	54.4	300	18	US-10-849-989-42	Sequence 90, Appli
33	181	54.4	300	18	US-10-712-124-90	Sequence 2, Appli
34	181	54.4	314	9	US-09-206-576-2	Sequence 24, Appli
35	181	54.4	314	10	US-09-983-000A-24	Sequence 227, App
36	181	54.4	314	14	US-10-097-340-227	Sequence 172, App
37	181	54.4	314	14	US-10-171-311-172	Sequence 303, App
38	181	54.4	314	14	US-10-303-583-1	Sequence 336, App
39	181	54.4	314	14	US-10-205-823-303	Sequence 143, App
40	181	54.4	314	14	US-10-177-293-336	Sequence 60, Appli
41	181	54.4	314	14	US-10-241-220-60	Sequence 2, Appli
42	181	54.4	314	14	US-10-301-822-143	Sequence 1, Appli
43	181	54.4	314	14	US-10-376-383-2	Sequence 1, Appli
44	181	54.4	314	14	US-10-239-555A-1	Sequence 1, Appli
45	181	54.4	314	15	US-10-220-107-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-220-107-6
; Sequence 6, Application US/10220107
; Publication No. US20040034193A1
; GENERAL INFORMATION:
; APPLICANT: Ashkar, Samy
; APPLICANT: Hikita, Sherry
; APPLICANT: Dehnl, Ghassan
; TITLE OF INVENTION: Biosynthetic Oncolytic Molecules and Uses Therefor
; FILE REFERENCE: CMCC 725
; CURRENT APPLICATION NUMBER: US/10/220,107
; CURRENT FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-220-107-6

Query Match 70.9%; Score 236; DB 15; Length 87;
Best Local Similarity 86.8%; Pred. No. 4.4e-17;
Matches 46; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
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Db 41 TPVPTVTDYDGRGDSVYVGLRSK-----PAGAGGAGPAGPAGPAGP 87
RESULT 2
US-10-900-512-6
; Sequence 6, Application US/10900512

; TITLE OF INVENTION: diseases
; FILE REFERENCE: WO 473
; CURRENT APPLICATION NUMBER: US/10/477,876
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 0111296
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-477-876-3

Query Match 54.4%; Score 181; DB 16; Length 286;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRP 40
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Db 114 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRP 149

RESULT 6

US-10-097-340-231
; Sequence 231, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT

; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer

; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-231

Query Match 54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 115 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRP 150

RESULT 7

US-10-171-311-176
; Sequence 176, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerah, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-176

Query Match 54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFRP 40
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Db 115 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRP 150

RESULT 8

US-10-205-823-307
; Sequence 307, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25

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; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 307
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-307

Query Match          54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRRSKSKKFRRP 40
    |||||
Db 115 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 150

RESULT 9
US-10-177-293-340
; Sequence 340, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Fustai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-340
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Query Match          54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRRSKSKKFRRP 40
    |||||
Db 115 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 150

RESULT 10
US-10-301-822-147
; Sequence 147, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kanatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-147

Query Match          54.4%; Score 181; DB 14; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRRSKSKKFRRP 40
    |||||
Db 115 ATEVFTPVVPTVDTYDGRGDSVVYGLRSKSKKFRRP 150

RESULT 11
US-10-678-355-6
; Sequence 6, Application US/10678355
; Publication No. US20040142865A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Georg F.
; TITLE OF INVENTION: OSTEOPOINTIN-BASED CANCER THERAPIES
; FILE REFERENCE: 00398-148001
; CURRENT APPLICATION NUMBER: US/10/678,355
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,712
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-678-355-6

Query Match          54.4%; Score 181; DB 16; Length 287;
Best Local Similarity 97.2%; Pred. No. 7.8e-11;
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Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVTDYDGRGDSVVYGRSKSKKFRFP 40
|||||
Db 115 ATEVFTPVVPTVTDYDGRGDSVVYGLRSKSKKFRFP 150
|||||

RESULT 12

US-10-187-975-48
; Sequence 48, Application US/10187975
; Publication No. US20030224982A1
; GENERAL INFORMATION:

; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh
; APPLICANT: Patturajan, Meera
; APPLICANT: Ellerman, Karen
; APPLICANT: Gorman, Linda
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elna
; APPLICANT: Spytek, Kimberly
; APPLICANT: Miller, Charles
; APPLICANT: Edinger, Shlomit
; APPLICANT: Hjal, Tord
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Baumgartner, Jason
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Pena, Carol
; APPLICANT: Chapoval, Andrei
; APPLICANT: Rastelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Vernte, Corine
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: 21402-397A
; CURRENT APPLICATION NUMBER: US/10/187,975
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303,046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/303,828
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/304,502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305,011
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,262
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/305,673
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/306,085
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 60/307,536
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/308,228
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/308,877
; PRIOR FILING DATE: 2001-07-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 48
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-187-975-48

Query Match 54.4%; Score 181; DB 15; Length 290;
Best Local Similarity 97.2%; Pred. No. 7.9e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVTDYDGRGDSVVYGRSKSKKFRFP 40
|||||
Db 142 ATEVFTPVVPTVTDYDGRGDSVVYGLRSKSKKFRFP 177
|||||

RESULT 13

US-10-477-876-2
; Sequence 2, Application US/10477876
; Publication No. US20040235720A1
; GENERAL INFORMATION:
; APPLICANT: Applied Research Systems ARS Holding N.V.
; TITLE OF INVENTION: Use of osteopontin for the treatment and/or prevention of demyel
; FILE REFERENCE: WO 473
; CURRENT APPLICATION NUMBER: US/10/477,876
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 01111296
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-477-876-2

Query Match 54.4%; Score 181; DB 16; Length 299;
Best Local Similarity 97.2%; Pred. No. 8.1e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVTDYDGRGDSVVYGRSKSKKFRFP 40
|||||
Db 127 ATEVFTPVVPTVTDYDGRGDSVVYGLRSKSKKFRFP 162
|||||

RESULT 14

US-09-919-770-2
; Sequence 2, Application US/09919770
; Patent No. US20020048577A1
; GENERAL INFORMATION:
; APPLICANT: Bornstein, Paul
; APPLICANT: Kyriakides, Themis
; APPLICANT: Ratner, Buddy
; APPLICANT: Giachelli, Cecilia
; APPLICANT: Martinson, Laura
; APPLICANT: Scatena, Marta
; TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response
; FILE REFERENCE: UOPW117618
; CURRENT APPLICATION NUMBER: US/09/919,770
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,071
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-919-770-2

Query Match 54.4%; Score 181; DB 9; Length 300;
Best Local Similarity 97.2%; Pred. No. 8.2e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATEVFTPVVPTVTDYDGRGDSVVYGRSKSKKFRFP 40
|||||
Db 128 ATEVFTPVVPTVTDYDGRGDSVVYGLRSKSKKFRFP 163
|||||

Thu Jul 28 09:37:20 2005

```
RESULT 15
US-10-097-340-229
; Sequence 229, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHWANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 229
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-229

Query Match      54.4%; Score 181; DB 14; Length 300;
Best Local Similarity 97.2%; Pred. No. 8.2e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 ATEVETPVVPTVDTYDGRGDSVVYGRSKSKKFRPP 40
      |||||||
Db      128 ATEVETPVVPTVDTYDGRGDSVVYGLRSKSKKFRPP 163

Search completed: July 27, 2005, 18:28:26
Job time : 155 secs
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:05:17 ; Search time 39 Seconds
(without alignments)
155.427 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

Sequence: 1 RSRRATEVFTPVVPTVDTYD.....AGGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	181	54.4	314	1	S09575	osteopontin precur
2	128.5	38.6	303	1	GEPCO	osteopontin precur
3	121.5	36.5	311	1	JC1191	osteopontin precur
4	118	35.4	278	1	JS0638	osteopontin precur
5	114	34.2	407	2	G90907	probable tail fibe
6	113	33.9	294	1	A37818	osteopontin precur
7	111	33.3	301	2	JCS811	osteopontin - rat
8	111	33.3	317	1	A25917	osteopontin precur
9	107.5	32.3	366	2	S11449	collagen short cha
10	107.5	32.3	423	2	A41207	collagen 13, nonfi
11	98	29.4	1039	2	T35878	hypothetical prote
12	97	29.1	437	2	H90854	probable tail fibe
13	97	29.1	439	2	C90769	probable tail fibe
14	96	28.8	1464	2	S59856	collagen alpha 1(I
15	95.5	28.7	1464	1	CGHU1S	collagen alpha 1(I
16	95.5	28.7	1486	1	B40333	collagen alpha 1(I
17	95	28.5	283	2	T32921	hypothetical prote
18	95	28.5	294	2	T29838	hypothetical prote
19	94	28.2	437	2	H90877	probable tail fibe
20	94	28.2	437	2	E90996	probable tail fibe
21	94	28.2	439	2	A85719	probable tail fibe
22	94	28.2	439	2	A85741	probable tail fibe
23	93	27.9	283	2	T29837	hypothetical prote
24	93	27.9	294	2	T29839	hypothetical prote
25	93	27.9	375	2	G85631	hypothetical prote
26	93	27.9	423	2	C75434	SLH family protein
27	93	27.9	437	2	E90968	probable tail fibe
28	93	27.9	438	2	S53787	collagen alpha cha
29	93	27.9	439	2	E85816	probable tail fibe

30	92.5	27.8	316	2	T20497	hypothetical prote
31	92	27.6	228	2	A44982	collagen UC001 - p
32	92	27.6	473	2	I50829	collagen - chicken
33	92	27.6	1042	1	CGCH1S	collagen alpha 1(I
34	92	27.6	1453	2	S21626	collagen alpha 1(I
35	91.5	27.5	291	2	T20942	hypothetical prote
36	91.5	27.5	886	2	I50694	collagen alpha 1(I
37	91.5	27.5	1049	1	CGBO7S	collagen alpha 1(I
38	91.5	27.5	1366	1	CGHU2S	collagen alpha 2(I
39	91	27.3	145	2	T08435	la costa protein -
40	91	27.3	301	2	B31219	collagen 2 - Caeno
41	90.5	27.2	103	2	C34770	ORF3 protein - sai
42	90.5	27.2	460	2	T33110	hypothetical prote
43	90.5	27.2	779	1	CGBO1S	collagen alpha 1(I
44	90	27.0	286	2	S34665	collagen, cuticula
45	90	27.0	297	2	T27525	hypothetical prote

ALIGNMENTS

RESULT 1

S09575

osteopontin precursor, splice form A - human

N;Alternate names: bone sialoprotein I; lactopontin; milk protein, 75K; secreted phosph N;Contains: osteopontin, splice form B; osteopontin, splice form C

C;Species: Homo sapiens (man)

C;Date: 20-May-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Accession: S50028; S09575; A35326; JQ1529; I56986; I76601; I76602; A41802; S04505

R;Hijsya, N.; Setoguchi, M.; Matsuura, K.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.

Biochem. J. 303, 255-262, 1994

A;Title: Cloning and characterization of the human osteopontin gene and its promoter.

A;Reference number: S50028; MUID:95031968; PMID:7945249

A;Accession: S50028

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-314 <HID>

A;Cross-references: UNIPROT:PI0451; EMBL:DI4813; NID:g506341; PIDN:BAA03554.1; PID:g506

A;Note: the authors translated the codon GTG for residue 5 as Tyr

R;Kiefer, M.C.; Bauer, D.M.; Barr, P.J.

Nucleic Acids Res. 17, 3306, 1989

A;Title: The cDNA and derived amino acid sequence for human osteopontin.

A;Reference number: S09575; MUID:89263749; PMID:2726470

A;Accession: S09575

A;Molecule type: mRNA

A;Residues: 1-314 <KIE>

A;Cross-references: EMBL:X13694; NID:g935147; PIDN:CAA31984.1; PID:g35148

R;Young, M.F.; Kerr, J.M.; Termini, J.D.; Wewer, U.M.; Ge Wang, M.; McBride, O.W.; Fish

Genomics 7, 491-502, 1990

A;Title: cDNA cloning, mRNA distribution and heterogeneity, chromosomal location, and R

A;Reference number: A35326; MUID:90353945; PMID:1974876

A;Accession: A35326

A;Molecule type: mRNA

A;Residues: 1-58,73-314 <YOU>

A;Cross-references: GB:J04765; NID:g189404; PIDN:AAA59974.1; PID:g189405

R;Kohri, K.; Suzuki, Y.; Yoshida, K.; Yamamoto, K.; Amasaki, N.; Yamate, T.; Umekawa, T

Biochem. Biophys. Res. Commun. 184, 859-864, 1992

A;Title: Molecular cloning and sequencing of cDNA encoding urinary stone protein, which

A;Reference number: JQ1529; MUID:92246977; PMID:1575754

A;Accession: JQ1529

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 67-273 <KOH>

A;Experimental source: kidney

R;Saitoh, Y.; Kuratsu, J.; Takeshima, H.; Yamamoto, S.; Ushio, Y.

Lab. Invest. 72, 55-63, 1995

A;Title: Expression of osteopontin in human glioma. Its correlation with the malignancy

A;Reference number: I56986; MUID:95139605; PMID:7837791

A;Accession: I56986

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-187,'H',189-236,'A',238-314 <SAIL>

A;Cross-references: GB:D28759; NID:g633074; PIDN:BAA05949.1; PID:g992948

A:Accession: I76601
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-57,72-187,'H','189-236','A',238-314 <SAI2>
A:Cross-references: GB:D28760; NID:g633075; PIDN:BAA05950.1; PID:g992949
A:Accession: I76602
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-31,59-187,'H','189-236','A',238-314 <SAI3>
A:Cross-references: GB:D28761; NID:g633076; PIDN:BAA05951.1; PID:g992950
R:Shiraga, H.; Min, W.; VanDusen, W.J.; Clayman, M.D.; Miner, D.; Terrell, C.H.; Sherbot
Proc. Natl. Acad. Sci. U.S.A. 89, 426-430, 1992
A:Title: Inhibition of calcium oxalate crystal growth in vitro by uropontin: another mem
A:Reference number: A41802; MUID:92108068; PMID:1729712
A:Accession: A41802
A:Molecule type: protein
A:Residues: 19-62 <SHI>
R:Senger, D.R.; Perruzzi, C.A.; Papadopoulos, A.; Tenen, D.G.
Biochim. Biophys. Acta 996, 43-48, 1989
A:Title: Purification of a human milk protein closely similar to tumor-secreted phosphop
A:Reference number: S04505; MUID:89287357; PMID:2736258
A:Accession: S04505
A:Status: preliminary
A:Molecule type: protein
A:Residues: 17-23;169-182 <SEN>
C:Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,
C:Genetics:
A:Gene: GDB:SPPI; BNSP; OPN
A:Cross-references: GDB:118889; OMIM:166490
A:Map position: 4q21-q25
C:Superfamily: osteopontin
C:Keywords: alternative splicing; bone; cell binding; extracellular matrix; phosphoprote
F:1-314/Product: osteopontin precursor, splice form A #status predicted <PRA>
F:1-57,72-314/Product: osteopontin precursor, splice form B #status predicted <PRB>
F:1-31,59-314/Product: osteopontin precursor, splice form C #status predicted <PRC>
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-314/Product: osteopontin #status predicted <MAT>
F:86-95/Region: aspartic acid-rich
F:159-163/Region: cell attachment (R-G-D) motif
F:24,26,27,62,63,191,234,303,308,310/Binding site: phosphate (Ser) (covalent) #statu
F:79,106/Binding site: carboxylate (Asn) (covalent) #status predicted
F:185/Binding site: phosphate (Thr) (covalent) #status predicted
Query Match 54.4%; Score 181; DB 1; Length 314;
Best Local Similarity 97.2%; Pred. No. 1.2e-10;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKSKFRP 40
DB 142 ATEVFTPVVPTVDYDGRGDSVVYGLRSKSKFRP 177
RESULT 2
GEPGO
osteopontin precursor - pig
N:Alternate names: bone sialoprotein I; phosphoprotein I, secreted
N:Contains: 20K glycoprotein; 23K glycoprotein
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S14903; A35204; S24372; S06690
R:Wrana, J.L.; Zhang, Q.; Sodek, J.
Nucleic Acids Res. 17, 10119, 1989
A:Title: Full length cDNA sequence of porcine secreted phosphoprotein-I (SPP-I, osteopon
A:Reference number: S14903; MUID:90098793; PMID:2602123
A:Accession: S14903
A:Molecule type: mRNA
A:Residues: 1-303 <WRA>
A:Cross-references: UNIPROT:P14287; EMBL:X16575; NID:g2120; PIDN:CAA34594.1; PID:g2121
R:Zhang, Q.; Domenicucci, C.; Goldberg, H.A.; Wrana, J.L.; Sodek, J.
J. Biol. Chem. 265, 7583-7589, 1990
A:Title: Characterization of fetal porcine bone sialoproteins, secreted phosphoprotein I
is derived from the carboxyl terminus of SPP-I.
A:Reference number: A35204; MUID:90237064; PMID:2332443

A:Accession: A35204
A:Molecule type: protein
A:Residues: 17-36;172-211 <ZHA>
R:Zhang, Q.; Wrana, J.L.; Sodek, J.
Eur. J. Biochem. 207, 649-659, 1992
A:Title: Characterization of the promoter region of the porcine opn (osteopontin, secret
omoter.
A:Reference number: S24372; MUID:92339454; PMID:1633816
A:Accession: S24372
A:Molecule type: DNA
A:Residues: 1-18 <ZH2>
A:Cross-references: EMBL:M84121; NID:gi64599; PIDN:AAA31094.1; PID:gi64600
C:Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,
C:Superfamily: osteopontin
C:Keywords: bone; cell binding; extracellular matrix; phosphoprotein; sialoglycoprotein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-303/Product: osteopontin #status experimental <MAT>
F:86-93/Region: aspartic acid-rich
F:154-156/Region: cell attachment (R-G-D) motif
F:172-303/Product: 23K glycoprotein #status experimental <23K>
F:193-303/Product: 20K glycoprotein #status experimental <20K>
F:79/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 38.6%; Score 128.5; DB 1; Length 303;
Best Local Similarity 80.0%; Pred. No. 1.6e-05;
Matches 28; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 5 ATEVFTPVVPTVDYDGRGDSVVYGRSKSKFR 39
DB 138 ATDV-TPAVPTGDPNDGRGDSVVYGLRSKSKFR 171
RESULT 3
JC1191
osteopontin precursor - rabbit
N:Alternate names: bone sialoprotein I; secreted phosphoprotein I
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: JC1191; S54977; S54976
R:Tezuka, K.; Sato, T.; Kamioka, H.; Nijweide, P.J.; Tanaka, K.; Matsuo, T.; Ohta, M.;
Biochem. Biophys. Res. Commun. 186, 911-917, 1992
A:Title: Identification of osteopontin in isolated rabbit osteoclasts.
A:Reference number: JC1191; MUID:92360044; PMID:1379809
A:Accession: JC1191
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-311 <TEZ>
A:Cross-references: UNIPROT:P31097; DDBJ:D11411; NID:g217735; PIDN:BAA01993.1; PID:g2177
A:Note: the authors translated the codon TCT for residue 126 as Glu and GAC for residue
R:Nasu, K.; Ishida, T.; Setoguchi, M.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.
Biochem. J. 307, 257-265, 1995
A:Title: Expression of wild-type and mutated rabbit osteopontin in Escherichia coli, an
A:Reference number: S54977; MUID:95234045; PMID:7717985
A:Accession: S54977
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 78-84,'V','86-99','Q','101-128','SDE','129-150','I',152-166 <NAS>
A:Cross-references: EMBL:D16544
R:Nasu, K.; Ishida, T.; Hijiyu, N.; Setoguchi, M.; Akizuki, S.; Higuchi, Y.; Yamamoto, S.
submitted to the EMBL Data Library, September 1994
A:Description: Molecular cloning of rabbit osteopontin cDNA and its expression.
A:Reference number: S54976
A:Accession: S54976
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-84,'V','86-99','Q','101-128','SDE','129-150','I',152-311 <NA2>
A:Cross-references: EMBL:D16544; NID:g538244; PIDN:BAA03980.1; PID:g538245
C:Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,
C:Genetics:
A:Gene: OC-1
C:Superfamily: osteopontin
C:Keywords: bone; cell binding; extracellular matrix; phosphoprotein; sialoglycoprotein
F:1-16/Domain: signal sequence #status predicted <SIG>

A;Residues: 1-42, 'P', 44-294 <PAT>
A;Cross-references: EMBL:L16151; NID:g50863; PIDN:CRA34276.1; PID:g50864
R;Singh, R.P.; Fatarca, R.; Schwartz, J.; Singh, P.; Cantor, H.
J. Exp. Med. 171, 1931-1942, 1990
A;Title: Definition of a specific interaction between the early T lymphocyte activation
A;Reference number: A60931; MUID:90278349; PMID:2351930
A;Accession: A60931
A;Molecule type: protein
A;Residues: 158-176 <SIN>
A;Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,
C;Genetics:
A;Gene: Eta-1
A;Map position: 5
A;Introns: 18/3; 30/3; 57/3; 71/3; 165/3
C;Superfamily: osteopontin
C;Keywords: bone; cell binding; extracellular matrix; phosphoprotein; sialoglycoprotein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-294/Product: osteopontin #status predicted <MAT>
F;85-96/Region: aspartic acid-rich
F;144-146/Region: cell attachment (R-G-D) motif
F;78/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.9%; Score 113; DB 1; Length 294;
Best Local Similarity 62.5%; Pred. No. 0.00052;
Matches 20; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 7 EVFTPVPTVDYDGRGDSVVYGRSKSKKF 38
: |||:|||||:|||||:|||||: |||: |||:
Db 129 DFTFTPIPTVDVDPNGRGLSLAYGLRSKRSF 160

RESULT 7
JC5811
osteopontin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
C;Accession: JC5811
R;Lasa, M.; Chang, P.L.; Prince, C.W.; Pinna, L.A.
Biochem. Biophys. Res. Commun. 240, 602-605, 1997
A;Title: Phosphorylation of osteopontin by Golgi apparatus casein kinase.
A;Reference number: JC5811; MUID:98063283; PMID:9398611
A;Accession: JC5811
A;Molecule type: protein
A;Residues: 1-301 <LAS>
A;Experimental source: brain
C;Comment: This protein is involved in the initiation of the bone calcification process,
ues, early resistance to bacterial infection and binding of tumor cells at secondary sit
C;Superfamily: osteopontin

Query Match 33.3%; Score 111; DB 2; Length 301;
Best Local Similarity 64.5%; Pred. No. 0.00083;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 7 EVFTPVPTVDYDGRGDSVVYGRSKSKKF 37
: |||:|||||:|||||:|||||: |||: |||:
Db 113 DVLTFPIPTVDVDPNGRGLSLAYGLRSKRSF 143

RESULT 8
A25917
osteopontin precursor - rat
N;Alternate names: bone sialoprotein I; phosphoprotein I, secreted; tumor-secreted phosph
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Dec-1987 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A25917; A45132; B45132; S28772; S04506; A45925
R;Oldberg, A.; Franzen, A.; Heinegard, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 8819-8823, 1986
A;Title: Cloning and sequence analysis of rat bone sialoprotein (osteopontin) cDNA revea
A;Reference number: A25917; MUID:87067405; PMID:3024151
A;Accession: A25917
A;Molecule type: mRNA
A;Residues: 1-317 <OLD>
A;Cross-references: UNIPROT:P08721; GB:M14656; NID:g205859; PIDN:AAA1762.1; PID:g205860

R;Singh, K.; Mukherjee, A.B.; De Vouge, M.W.; Mukherjee, B.B.
J. Biol. Chem. 267, 23847-23851, 1992
A;Title: Differential processing of osteopontin transcripts in rat kidney- and osteoblas
A;Reference number: A45132; MUID:93054745; PMID:1429723
A;Accession: A45132
A;Molecule type: protein
A;Residues: 36-51 <SIN1>
A;Experimental source: kidney
A;Note: sequence extracted from NCBI backbone (NCBIP:118869)
A;Accession: B45132
A;Molecule type: protein
A;Residues: 272-282 <SIN2>
A;Note: sequence extracted from NCBI backbone (NCBIP:118871)
R;Prince, C.W.; Oosawa, T.; Butler, W.T.; Tomana, M.; Bhowm, A.S.; Bhowm, M.; Schrohenlo
J. Biol. Chem. 262, 2900-2907, 1987
A;Title: Isolation, characterization, and biosynthesis of a phosphorylated glycoprotein
A;Reference number: S28772; MUID:87137549; PMID:3469201
A;Accession: S28772
A;Status: preliminary
A;Molecule type: protein
A;Residues: 17-26, 'X' <PRI>
R;Senger, D.R.; Perruzzi, C.A.; Papadopoulos, A.; Tenen, D.G.
Biochim. Biophys. Acta 996, 43-48, 1989
A;Title: Purification of a human milk protein closely similar to tumor-secreted phosphop
A;Reference number: S04505; MUID:89287357; PMID:2736258
A;Accession: S04506
A;Status: preliminary
A;Molecule type: protein
A;Residues: 17-26;155-167 <SEN>
R;Senger, D.R.; Perruzzi, C.A.; Gracey, C.F.; Papadopoulos, A.; Tenen, D.G.
Cancer Res. 48, 5770-5774, 1988
A;Title: Secreted phosphoproteins associated with neoplastic transformation: close homol
A;Reference number: A45925; MUID:89002730; PMID:3167835
A;Accession: A45925
A;Molecule type: protein
A;Residues: 17-25 <SE2>
C;Comment: This protein is an acidic glycoprotein rich in aspartic acid, glutamic acid,
C;Superfamily: osteopontin
C;Keywords: bone; cell binding; extracellular matrix; phosphoprotein; sialoglycoprotein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-317/Product: osteopontin #status predicted <MAT>
F;86-96/Region: aspartic acid-rich
F;144-146/Region: cell attachment (R-G-D) motif
F;79/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.3%; Score 111; DB 1; Length 317;
Best Local Similarity 64.5%; Pred. No. 0.00087;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 7 EVFTPVPTVDYDGRGDSVVYGRSKSKKF 37
: |||:|||||:|||||:|||||: |||: |||:
Db 129 DVLTFPIPTVDVDPNGRGLSLAYGLRSKRSF 159

RESULT 9
S11449
collagen short chain - freshwater sponge (Ephydatia muelleri) (fragment)
C;Species: Ephydatia muelleri
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S11449
R;Exposito, J.Y.; Ouazana, R.; Garrone, R.
Eur. J. Biochem. 190, 401-406, 1990
A;Title: Cloning and sequencing of a Porifera partial cDNA coding for a short-chain coll
A;Reference number: S11449; MUID:90306040; PMID:2163843
A;Accession: S11449
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-366 <EXP>
A;Cross-references: UNIPROT:P18503; EMBL:X52598; NID:g9297; PIDN:CAA36831.1; PID:g9298

Query Match 32.3%; Score 107.5; DB 2; Length 366;
Best Local Similarity 46.6%; Pred. No. 0.0022;
Matches 27; Conservative 2; Mismatches 10; Indels 19; Gaps 3;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 17:57:07 ; Search time 169 seconds
(without alignments)
190.893 Million cell updates/sec

Title: US-09-981-845-11

Perfect score: 333

Sequence: 1 RSRRAFEVTPVVTVDYD.....AGGPAGPAGPAGPAGPA 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	181	54.4	314	1	OSTP_HUMAN
2	128.5	38.6	105	2	Q9TSY3
3	128.5	38.6	303	1	OSTP_PIG
4	121.5	36.5	311	1	OSTP_RABIT
5	121	36.3	278	1	OSTP_SHEEP
6	118	35.4	213	2	Q91VH4
7	118	35.4	278	1	OSTP_BOVIN
8	118	35.4	279	2	Q641Z5
9	118	35.4	295	2	Q6PKX3
10	114	34.2	407	2	Q8X5F6
11	113	33.9	294	1	OSTP_MOUSE
12	111	33.3	165	2	Q6N617
13	111	33.3	317	1	OSTP_RAT
14	111	33.3	317	2	P97827
15	108	32.4	200	2	Q6X1Z9
16	108	32.4	358	2	Q9J3U4
17	107.5	32.3	366	1	CAS4_EPHMU
18	107.5	32.3	422	2	Q24893
19	104	31.2	180	2	Q7QNL4
20	104	31.2	191	2	Q7PNG8
21	99.5	29.9	1445	2	Q93251
22	99	29.7	1321	2	Q72202
23	98	29.4	306	2	Q9ACN2
24	98	29.4	1039	2	O50516
25	97.5	29.3	1355	1	CA21_RANCA
26	97	29.1	437	2	Q8X5D0
27	97	29.1	439	2	Q7AFX3
28	97	29.1	604	2	Q91252
29	96	28.8	479	2	Q91A62
30	96	28.8	998	2	Q8CFM4
31	96	28.8	1222	2	Q8K173

32	96	28.8	1464	1	CA13_MOUSE
33	96	28.8	1464	2	Q7TT32
34	96	28.8	1464	2	Q8BKY2
35	96	28.8	1464	2	Q8BLW4
36	95.5	28.7	1464	1	CA11_HUMAN
37	95.5	28.7	1486	2	Q91717
38	95.5	28.7	1486	2	Q7ZTI6
39	95	28.5	283	2	O44989
40	95	28.5	294	2	Q17459
41	94.5	28.4	809	2	Q93485
42	94.5	28.4	1346	2	Q801M5
43	94.5	28.4	1449	2	Q910C0
44	94	28.2	361	2	Q7AE98
45	94	28.2	437	2	Q9EVE8

ALIGNMENTS

RESULT 1

OSTP_HUMAN STANDARD; PRT; 314 AA.
AC F10451; Q15681; Q15682; Q15683; Q8NBK2; Q961Z1;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
DE 1) (SPP-1) (Urinary stone protein) (Nephropontin) (Uropontin).
GN Name=SPP1; Synonyms=OPN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=89263749; PubMed=2726470;
RA Kiefer M.C., Bauer D.M., Barr P.J.;
RT "The cDNA and derived amino acid sequence for human osteopontin.";
RL Nucleic Acids Res. 17:3306-3306(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=90353945; PubMed=1974876;
RA Young M.F., Kerr J.M., Termino J.D., Wewer U.M., Wang M.G.,
RA McBride O.W., Fisher L.W.;
RT "cDNA cloning, mRNA distribution and heterogeneity, chromosomal
RT location, and RFLP analysis of human osteopontin (OPN).";
RL Genomics 7:491-502(1990).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=92108068; PubMed=1729712;
RA Shiraga H., Min W., Vandusen W.J., Clayman M.D., Miner D.,
RA Terrell C.H., Sherbotie J.R., Foreman J.W., Przysiecki C.,
RA Neilson E.G., Hoyer J.R.;
RT "Inhibition of calcium oxalate crystal growth in vitro by uropontin:
RT another member of the aspartic acid-rich protein superfamily.";
Proc. Natl. Acad. Sci. U.S.A. 89:426-430(1992).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=95394452; PubMed=7665163;
RA Crosby A.H., Edwards S.J., Murray J.C., Dixon M.J.;
RT "Genomic organization of the human osteopontin gene: exclusion of the
RT locus from a causative role in the pathogenesis of dentinogenesis
RT imperfecta type II.";
Genomics 27:155-160(1995).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=95031968; PubMed=7945249;
RA Hijiyama N., Setoguchi M., Matsuura K., Higuchi Y., Akizuki S.,
RA Yamamoto S.;
RT "Cloning and characterization of the human osteopontin gene and its
RT promoter.";
Biochem. J. 303:255-262(1994).

P08121	mus musculus
Q7tt32	mus musculus
Q8bky2	mus musculus
Q8blw4	mus musculus
P02452	homo sapiens
Q91717	homo sapiens
Q7zt16	homo sapiens
O44989	caenorhabditis
O17459	caenorhabditis
Q93485	oncorhynchus
Q801m5	oncorhynchus
Q910c0	oncorhynchus
Q7ae98	escherichia
Q9eve8	escherichia

[6] SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
RX MEDLINE=95139605; PubMed=7837791;
RA Saitoh Y., Kuratsu J., Takeshima H., Yamamoto S., Ushio Y.;
RT "Expression of osteopontin in human glioma. Its correlation with the
RL malignancy.";
RL Lab. Invest. 72:55-63(1995).
RN [7]
RN SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Brain;
RA Yu W., Sarginson J., Gibbs R.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RN SEQUENCE FROM N.A. (ISOFORM D).
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Negai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takenoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Okaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [9]
RN SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC TISSUE=Brain, and Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Masius K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywiniski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RN SEQUENCE OF 67-278 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92246977; PubMed=1575754;
RA Kohri K., Suzuki Y., Yoshida K., Yamamoto K., Amasaki N., Yamate T.,
RA Umekawa T., Iguchi M., Sinohara H., Kurita T.;
RT "Molecular cloning and sequencing of cDNA encoding urinary stone
RT protein, which is identical to osteopontin.";
RL Biochem. Biophys. Res. Commun. 184:859-864(1992).
CC [-] FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
CC integral part of the mineralized matrix. Probably important to
CC cell-matrix interaction.
CC [-] FUNCTION: Acts as a cytokine involved in enhancing production of
CC interferon-gamma and interleukin-12 and reducing production of
CC interleukin-10 and is essential in the pathway that leads to type
CC I immunity (By similarity).
CC [-] SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC [-] SUBCELLULAR LOCATION: Secreted.
CC [-] ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=A; Synonyms=OPN-a, OP1B;
CC IsoId=PI0451-1; Sequence=Displayed;
CC Name=B; Synonyms=OPN-b, OP1A;
CC IsoId=PI0451-2; Sequence=VSP_003778;
CC Name=C; Synonyms=OPN-c;
CC IsoId=PI0451-3; Sequence=VSP_003777;
CC Name=D;
CC IsoId=PI0451-4; Sequence=VSP_011639;
CC [-] PTM: Extensively phosphorylated on serine residues.
CC [-] PTM: N- and O-glycosylated.
CC [-] DISEASE: This protein plays a principal role in urinary stone
CC formation as the stone matrix.
CC [-] SIMILARITY: Belongs to the osteopontin family.
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X13694; AAA31984.1; -;
CC EMBL; J04765; AAA59974.1; -;
CC EMBL; M83248; AAA17675.1; -;
CC EMBL; U20758; AAA86886.1; -;
CC EMBL; D14813; BAA03554.1; -;
CC EMBL; D28759; BAA05949.1; -;
CC EMBL; D28760; BAA05950.1; -;
CC EMBL; D28761; BAA05951.1; -;
CC EMBL; AF052124; AAC28619.1; -;
CC EMBL; AK075463; BAC11635.1; -;
CC EMBL; BC007016; AAH07016.1; -;
CC EMBL; BC017387; AAH17387.1; -;
CC EMBL; BC022844; AAH22844.1; -;
CC PIR; S50038; S09575
CC GlycoSuiteDB; P10451; -;
CC GenSeq; HGNC:11255; SPPI.
CC H-InvDB; HIX0004361; -;
CC MIM; 166490; -;
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0005125; F:cytokine activity; ISS.
CC GO; GO:0008083; F:growth factor activity; TAS.
CC GO; GO:0005178; F:integrin binding; NAS.
CC GO; GO:0006916; F:anti-apoptosis; ISS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0007160; P:cell-matrix adhesion; NAS.
CC GO; GO:0030595; P:immune cell chemotaxis; TAS.
CC GO; GO:0005093; P:induction of positive chemotaxis; TAS.
CC GO; GO:0005050; P:negative regulation of bone mineralization; NAS.
CC GO; GO:0001503; P:proliferation; TAS.
CC GO; GO:0042102; P:regulation of myeloid blood cell differenti. . . ; TAS.
CC GO; GO:0045637; P:regulation of myeloid blood cell differenti. . . ; TAS.
CC GO; GO:0042088; P:T-helper 1 type immune response; TAS.
CC InterPro; IPR002038; Osteopontin.

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DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.

Query Match          54.4%; Score 181; DB 1; Length 314;
Best Local Similarity 97.2%; Pred. No. 4e-10;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ATEVFTVPVPTVDTYDGRGDSVVYGRSKSKKFRP 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 142 ATEVFTVPVPTVDTYDGRGDSVVYGLRSKSKKFRP 177

RESULT 2
Q9TSY3 ID Q9TSY3 PRELIMINARY; PRT; 105 AA.
AC Q9TSY3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Osteopontin (Fragment).
GN Name=Sppl;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20078367; PubMed=10612243;
RA Knoll A., Stratil A., Cepica S., Dvorak J.;
RT "Length polymorphism in an intron of the porcine osteopontin (SPPI)
RT gene is caused by the presence or absence of a SINE (PRE-1) element.";
RL Anim. Genet. 30:466-466(1999).
DR EMBL; AJ237667; CAB61259.1; -.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0001503; P:ossification; IEA.
DR InterPro; IPR002038; Osteopontin.
DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 1489 MW; F2FDCBAE560773CB CRC64;

Query Match          38.6%; Score 128.5; DB 2; Length 105;
Best Local Similarity 80.0%; Pred. No. 2.3e-05;
Matches 28; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 5 ATEVFTVPVPTVDTYDGRGDSVVYGRSKSKKFRP 39
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 ATDV-TPAVPTGPDNDGRGDSVVYGLRSKSKKFRP 42

RESULT 3
ID OSTP_PIG STANDARD; PRT; 303 AA.
AC F14287;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
DE 1) (SPPI-1).
GN Name=SPPI; Synonyms=OPN;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Bone;
RX MEDLINE=90098793; PubMed=2602123;
RA Wrana J.L., Zhang Q., Sodek J.;
RT "Full length cDNA sequence of porcine secreted phosphoprotein-I (SPPI,
RT osteopontin).";
RL Nucleic Acids Res. 17:10119-10119(1989).

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RN SEQUENCE OF 1-18 FROM N.A.
RX MEDLINE=92339454; PubMed=1633816;
RA Zhang Q., Wrana J.L., Sodek J.;
RT "Characterization of the promoter region of the porcine opn
RT (osteopontin, secreted phosphoprotein 1) gene. Identification of
RT positive and negative regulatory elements and a 'silent' second
RT promoter.";
RL Eur. J. Biochem. 207:649-659(1992).
RN [3]
SEQUENCE OF 17-36 AND 172-211.
RX TISSUE=Bone;
RC MEDLINE=90237064; PubMed=2332443;
RA Zhang Q., Domenicucci C., Goldberg H.A., Wrana J.L., Sodek J.;
RT "Characterization of fetal porcine bone sialoproteins, secreted
RT phosphoprotein I (SPPI, osteopontin), bone sialoprotein, and a 23-kDa
RT glycoprotein. Demonstration that the 23-kDa glycoprotein is derived
RT from the carboxyl terminus of SPPI.";
RL J. Biol. Chem. 265:7583-7589(1990).
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
CC integral part of the mineralized matrix. Probably important to
CC cell-matrix interaction.
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of
CC interferon-gamma and interleukin-12 and reducing production of
CC interleukin-10 and is essential in the pathway that leads to type
CC I immunity (By similarity).
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Extensively phosphorylated on serine residues.
CC -!- PTM: N- and O-glycosylated.
CC -!- SIMILARITY: Belongs to the osteopontin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X16575; CAA34594.1; -.
DR EMBL; M84121; AAA31094.1; -.
DR PIR; S14903; GEPGO.
DR GO; GO:0005578; C:extracellular matrix; ISS.
DR GO; GO:000125; F:cytokine activity; ISS.
DR GO; GO:0008083; F:growth factor activity; ISS.
DR GO; GO:0005178; F:integrin binding; ISS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0007160; P:cell-matrix adhesion; ISS.
DR GO; GO:0030595; P:immune cell chemotaxis; ISS.
DR GO; GO:0050930; P:induction of positive chemotaxis; ISS.
DR GO; GO:0030502; P:negative regulation of bone mineralization; ISS.
DR GO; GO:0042102; P:positive regulation of T-cell proliferation; ISS.
DR GO; GO:0045637; P:regulation of myeloid blood cell differenti...; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro; IPR002038; Osteopontin.
DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.
DR SMART; SM00017; OSTEO; 1.
DR PROSITE; PS00884; OSTEOPONTIN; 1.
KW Bion mineralization, Cell adhesion; Cytokine; Direct protein sequencing;
KW Glycoprotein; Phosphorylation; Sialic acid; Signal.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 303 Osteopontin.
FT SITE 154 156 Cell attachment site.
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 303 AA; 33668 MW; 87D6240E24013EF7 CRC64;

Query Match          38.6%; Score 128.5; DB 1; Length 303;
Best Local Similarity 80.0%; Pred. No. 6.5e-05;
Matches 28; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

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QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFR 39
DB 138 ATDV-TPAVPTGDPNDGRGDSVVYGLRSKSKKFR 171

RESULT 4
OSTP_RABBIT
ID OSTP_RABBIT STANDARD; PRT; 311 AA.
AC F31097; P46631;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
1) (SPP-1) (OC-1).
GN Name=SPP1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Osteoclast;
RX MEDLINE=92360044; PubMed=1379809;
RA Tezuka K.-I., Sato T., Kamioka H., Nijweide P.J., Tanaka K.,
RA Matsuo T., Ohta M., Kurihara N., Hakeda Y., Kumegawa M.;
RT "Identification of osteopontin in isolated rabbit osteoclasts.";
RN Biochem. J. 307:257-265(1995).
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
integral part of the mineralized matrix. Probably important to
cell-matrix interaction.
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of
interferon-gamma and interleukin-12 and reducing production of
interleukin-10 and is essential in the pathway that leads to type
I immunity (By similarity).
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Extensively phosphorylated on serine residues.
CC -!- PTM: N- and O-glycosylated.
CC -!- SIMILARITY: Belongs to the osteopontin family.
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CC
CC EMBL; D11411; BAA01993.1; -.
CC EMBL; D16544; BAA03980.1; -.
CC PIR; JC1191; JC1191.
CC InterPro; IPR002038; Osteopontin.
CC Pfam; PF00865; Osteopontin; 1.
CC PRINTS; PR00216; OSTEOPTNTN.
CC SMART; SM00017; OSTEO; 1.
CC PROSITE; PS00884; OSTEOPTNTN; 1.
KW Biomineralization; Cell adhesion; Cytokine; Glycoprotein;
KW Phosphorylation; Sialic acid; Signal.
FT SIGNAL 1 16 By similarity.
FT CHAIN 17 311 Osteopontin.
FT SITE 155 157 Cell attachment site.
FT CARBOHYD 103 103 N-linked (GlcNAc...) (Potential).
FT CONFLICT 85 85 M -> V (in Ref. 2).
FT CONFLICT 100 100 R -> Q (in Ref. 2).
FT CONFLICT 128 128 E -> ESDE (in Ref. 2).

QY 5 ATEVFTPVVPTVDTYDGRGDSVVYGRSKSKKFP 37
DB 138 ATTFTVETVPTVETVYDGRGDSVAVRLKRSKMF 171

Query Match 36.5%; Score 121.5; DB 1; Length 311;
Best Local Similarity 76.5%; Pred. No. 0.00033;
Matches 26; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

RESULT 5
OSTP_SHEEP
ID OSTP_SHEEP STANDARD; PRT; 278 AA.
AC Q9XSY9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
1) (SPP-1).
GN Name=SPP1; Synonyms=OPN;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RX MEDLINE=99423513; PubMed=10491620;
RA Johnson G.A., Spencer T.E., Burghardt R.C., Bazer F.W.;
RT "Ovine osteopontin: I. Cloning and expression of messenger ribonucleic
acid in the uterus during the periimplantation period.";
RN Biol. Reprod. 61:884-891(1999).
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
integral part of the mineralized matrix. Probably important to
cell-matrix interaction.
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of
interferon-gamma and interleukin-12 and reducing production of
interleukin-10 and is essential in the pathway that leads to type
I immunity (By similarity).
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Extensively phosphorylated on serine residues (By
similarity).
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the osteopontin family.
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or send an email to license@isb-sib.ch).
CC
CC EMBL; AF152416; AAD38388.1; -.
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0005125; F:cytokine activity; ISS.
CC InterPro; IPR002038; Osteopontin.
CC Pfam; PF00865; Osteopontin; 1.
CC PRINTS; PR00216; OSTEOPTNTN.
CC SMART; SM00017; OSTEO; 1.
CC PROSITE; PS00884; OSTEOPTNTN; 1.
KW Biomineralization; Cell adhesion; Cytokine; Glycoprotein;
KW Phosphorylation; Sialic acid; Signal.
FT SIGNAL 1 16 By similarity.
FT CHAIN 17 278 Osteopontin.
FT SITE 152 154 Cell attachment site.
FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).
FT CONFLICT 278 AA; 31052 MW; 37D49E1DD1FBFD47 CRC64;
SQ SEQUENCE 278 AA; 31052 MW; 37D49E1DD1FBFD47 CRC64;

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Query Match 36.3%; Score 121; DB 1; Length 278;
 Best Local Similarity 75.0%; Pred. No. 0.00033;
 Matches 24; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 8 VFTPTVPTVDTYDGRGDSVVYGRSKSKKPR 39
 ||||| || ||||| || ||||| || ||||| || |||||
 DB 138 VFTPTPTPTSTNDRGDSVAYGLKSKSKKPR 169

RESULT 6

Q91VH4 PRELIMINARY; PRT; 213 AA.
 AC Q91VH4;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN Names=Pogz;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zerbey B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Krzywinski M.I., Skaleka U., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Rodriguez A.C., Grimwood J., Smillius D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
 RL Strausberg R.;
 DR EMBL, BC014284; AAH14284.1; -;
 DR MGD; MG1:2442117; Pogz.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR GO; GO:0001503; P:ossification; IEA.
 DR Pfam; PF00865; Osteopontin; 1.
 DR PRINTS; PR00216; OSTEOPONTIN.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 213 AA; 23625 MW; 50CCESDDSE9E1797 CRC64;

Query Match 35.4%; Score 118; DB 2; Length 213;
 Best Local Similarity 65.6%; Pred. No. 0.00051;
 Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 7 EYFTPTVPTVDTYDGRGDSVVYGRSKSKKPR 38
 : ||||| ||||| ||||| ||||| :
 DB 48 DTFTPTVPTVDPDGRGDSLAYGLSKSRFQ 79

RESULT 7

OSTP_BOVIN
 ID OSTP_BOVIN STANDARD; PRT; 278 AA.

AC P31096; Q8GSP56;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
 1) (SPP-1).
 GN Name=SPP1; Synonyms=OPN;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084141; PubMed=1721033; DOI=10.1016/0378-1119(91)90439-1;
 RA Kerr J.M., Fisher L.W., Termino J.D., Young M.F.;
 RT "The cDNA cloning and RNA distribution of bovine osteopontin.";
 RL Gene 108:237-243(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Korean; TISSUE=Kidney;
 RA Lee T.Y., Ju S.K., Nam M.S.;
 RT "Cloning of osteopontin (OPN) in Korean native cattle.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 17-22; 44-54; 168-182 AND 221-243.
 RC TISSUE=Milk;
 RX MEDLINE=93308294; PubMed=8320368;
 RA Soerensen E.S., Petersen T.E.;
 RT "Purification and characterization of three proteins isolated from the
 protease peptone fraction of bovine milk.";
 RL J. Dairy Res. 60:189-197(1993).
 RN [4]
 RP SEQUENCE OF 17-28, AND PHOSPHORYLATION.
 RX PubMed=8663267;
 RA Salih E., Zhou H.-Y., Glimcher M.J.;
 RT "Phosphorylation of purified bovine bone sialoprotein and osteopontin
 by protein kinases";
 RL J. Biol. Chem. 271:16897-16905(1996).
 RN [5]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RC TISSUE=Milk;
 RX MEDLINE=96117654; PubMed=8535240;
 RA Soerensen E.S., Hoeirup P., Petersen T.E.;
 RT "Posttranslational modifications of bovine osteopontin: identification
 of twenty-eight phosphorylation and three O-glycosylation sites.";
 RL Protein Sci. 4:2040-2049(1995).
 CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
 integral part of the mineralized matrix. Probably important to
 cell-matrix interaction.
 CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of
 interferon-gamma and interleukin-12 and reducing production of
 interleukin-10 and is essential in the pathway that leads to type
 I immunity (By similarity).
 CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Bone, inner ear, kidney, uterus, lung, brain,
 epidermis.
 CC -!- SIMILARITY: Belongs to the osteopontin family.
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 CC -----
 DR EMBL; M6236; AAA30462.1; -;
 DR EMBL; AF492837; AAL99081.1; -;
 DR GO; GO:0005576; C:extracellular; ISS.
 DR GO; GO:0005125; F:cytokine activity; ISS.
 DR InterPro; IPR002038; Osteopontin.

```
DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.
DR SMART; SM00017; OSTEO; 1.
DR PROSITE; PS00884; OSTEOPTNTIN; 1.
KW Biomimeralization; Cell adhesion; Cytokine; Direct protein sequencing;
KW Glycoprotein; Phosphorylation; Sialic acid; Signal.
FT SIGNAL 1 16
FT CHAIN 17 278 Osteopontin.
FT SITE 152 154 Cell attachment site.
FT MOD_RES 23 23 Phosphoserine.
FT MOD_RES 24 24 Phosphoserine.
FT MOD_RES 26 26 Phosphoserine.
FT MOD_RES 27 27 Phosphoserine.
FT MOD_RES 60 60 Phosphoserine.
FT MOD_RES 62 62 Phosphoserine.
FT MOD_RES 63 63 Phosphoserine.
FT MOD_RES 76 76 Phosphoserine.
FT MOD_RES 78 78 Phosphoserine.
FT MOD_RES 81 81 Phosphoserine.
FT MOD_RES 95 95 Phosphoserine.
FT MOD_RES 100 100 Phosphoserine.
FT MOD_RES 103 103 Phosphoserine.
FT MOD_RES 115 115 Phosphoserine.
FT MOD_RES 121 121 Phosphoserine.
FT MOD_RES 124 124 Phosphoserine.
FT MOD_RES 178 178 Phosphothreonine.
FT MOD_RES 184 184 Phosphoserine.
FT MOD_RES 188 188 Phosphoserine.
FT MOD_RES 205 205 Phosphoserine.
FT MOD_RES 210 210 Phosphoserine.
FT MOD_RES 233 233 Phosphoserine.
FT MOD_RES 240 240 Phosphoserine.
FT MOD_RES 245 245 Phosphoserine.
FT MOD_RES 256 256 Phosphoserine.
FT MOD_RES 267 267 Phosphoserine.
FT MOD_RES 272 272 Phosphoserine.
FT MOD_RES 274 274 Phosphoserine.
FT CARBOHYD 131 131 O-linked.
FT CARBOHYD 140 140 O-linked.
FT CARBOHYD 145 145 O-linked.
FT CONFLICT 27 27 S -> T (in Ref. 4).
FT CONFLICT 42 42 I -> T (in Ref. 2).
FT CONFLICT 56 56 T -> A (in Ref. 2).
SQ SEQUENCE 278 AA; 30946 MW; EAB6EA39A6DDBE6F CRC64;

Query Match 35.4%; Score 118; DB 1; Length 278;
Best Local Similarity 68.8%; Pred. No. 0.00066;
Matches 22; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 8 VFTPVPTVDTYDGRGDSVVYGRSKSKFRR 39
||| :||| :||| :||| :||| :||| :||| :|||
DB 138 VFTPTFTESANDGRGDSVAYGLKRSKFR 169

RESULT 8
ID Q64125 PRELIMINARY; PRT; 279 AA.
AC Q64125;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Early T-lymphocyte activator-1 (Fragment).
GN Name=Sppl; Synonyms=Eta-1/Op;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95272553; PubMed=7753053; DOI=10.1016/0161-5890(95)00053-H;
RA Ono M., Yamamoto T., Nose M.;
RT "Allelic difference in the nucleotide sequence of the Eta-1/Op gene transcript.";
```

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RL Mol. Immunol. 32:447-448(1995).
DR EMBL; S78177; AAB34351.2; -.
DR MGD; MGI:98389; Sppl.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0001503; P:ossification; IEA.
DR InterPro; IPR002038; Osteopontin.
DR Pfam; PF00865; Osteopontin; 1.
DR PRINTS; PR00216; OSTEOPONTIN.
DR SMART; SM00017; OSTEO; 1.
DR PROSITE; PS00884; OSTEOPTNTIN; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 279 AA; 30939 MW; BOEF5855D0AC14A2 CRC64;

Query Match 35.4%; Score 118; DB 2; Length 279;
Best Local Similarity 65.6%; Pred. No. 0.00067;
Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 7 EVFTPVPTVDTYDGRGDSVVYGRSKSKFRR 38
:|||||:|||||:|||||:|||||:
DB 114 DTFTFIVTVDVPGRGDSLAYGLRSKRSFQ 145

RESULT 9
ID Q6PKE3 PRELIMINARY; PRT; 295 AA.
AC Q6PKE3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002113; AA02113.1; -.
DR EMBL; BC080720; AA080720.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR002038; Osteopontin.
DR Pfam; PF00865; Osteopontin; 1.
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DR PRINTS; PR00216; OSTEOPOINTIN.
DR SMART; SM00017; OSTEO; 1.
DR PROSITE; PS00884; OSTEOPOINTIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 295 AA; 32652 MW; B06998BF87CF9A68 CRC64;
Query Match 35.4%; Score 118; DB 2; Length 295;
Best Local Similarity 65.6%; Pred. No. 0.0007;
Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 7 EVTPVPTVDTYDGRGDSVVYGRSKSKKFR 38
Db 130 DTPTPIPTVDTVPDGRGDSLAYLGRSKSRFQ 161
RESULT 10
Q8X5F6 PRELIMINARY; PRT; 407 AA.
ID Q8X5F6 PRELIMINARY; PRT; 407 AA.
AC Q8X5F6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative tail fiber protein.
GN OrderedLocuNames=ECS2231;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AP002557; BAB35654.1; -.
DR F01; G90907; G90907.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF06820; Phage fiber C; 1.
SQ SEQUENCE 407 AA; 41291 MW; D2F6C586ABEC3EB CRC64;
Query Match 34.2%; Score 114; DB 2; Length 407;
Best Local Similarity 48.6%; Pred. No. 0.0024;
Matches 34; Conservative 5; Mismatches 23; Indels 8; Gaps 4;
QY 1 RRRATEVTPVPTVDTYDGRGDSVVYGRSKSKKFR-----PAGAG--GPAGPAG 52
Db 234 QSRIAEEAVNRITPVVPGPKGPGAGPQKGDGKRGDTGPAGATGERGPAGDAG 293
QY 53 PAGPAGPAGP 62
Db 294 PAGPAGPAGP 303
RESULT 11
OSTP MOUSE
ID OSTP MOUSE STANDARD; PRT; 294 AA.
AC P10923; P10908;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein 1) (Secreted phosphoprotein
DE 1) (SPP-1) (Minopontin) (Early T lymphocyte activation 1 protein)
DE (2AR) (Calcium oxalate crystal growth inhibitor protein).
GN Name=Sppi; Synonyms=Bta-1, Op, Spp-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RA Cantor H.;
RT "Eta-1 (osteopontin): an early component of type-1 (cell-mediated)
RL Science 287:860-864 (2000).
CC -!- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
CC integral part of the mineralized matrix. Probably important to
CC cell-matrix interaction.
CC -!- FUNCTION: Acts as a cytokine involved in enhancing production of
CC interferon-gamma and interleukin-12 and reducing production of
CC interleukin-10 and is essential in the pathway that leads to type
CC I immunity.
CC -!- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Extensively phosphorylated on serine residues.
CC -!- PTM: N- and O-glycosylated.
CC -!- SIMILARITY: Belongs to the osteopontin family.
CC
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CC -----
CC EMBL; X51834; CAA36132.1; -;
CC EMBL; X13986; CAA32165.1; -;
CC DR EMBL; J04806; AAA57265.1; -;
CC DR EMBL; X16151; CAA34276.1; -;
CC DR EMBL; BC057858; AAH57858.1; -;
CC DR PIR; A37818; A37818.
CC MGD; MGI:98389; Spp1.
CC DR GO; GO:0005578; C:extracellular matrix; ISS.
CC DR GO; GO:0005125; F:cytokine activity; NAS.
CC DR GO; GO:0008083; F:growth factor activity; ISS.
CC DR GO; GO:0005178; F:integrin binding; ISS.
CC DR GO; GO:0006916; P:anti-apoptosis; NAS.
CC DR GO; GO:0007160; P:cell-matrix adhesion; ISS.
CC DR GO; GO:0030595; P:immune cell chemotaxis; ISS.
CC DR GO; GO:0050930; P:induction of positive chemotaxis; ISS.
CC DR GO; GO:0030502; P:negative regulation of bone mineralization; ISS.
CC DR GO; GO:0042102; P:positive regulation of T-cell proliferation; ISS.
CC DR GO; GO:0045637; P:regulation of myeloid blood cell differenti. . .; ISS.
CC DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
CC DR InterPro; IPR002038; Osteopontin.
CC DR Pfam; PF00865; Osteopontin; 1.
CC DR PRINTS; PR00216; OSTEOPONTIN.
CC DR PROSITE; PS00884; OSTEOPONTIN; 1.
CC KW Biomineralization; Cell adhesion; Cytokine; Direct protein sequencing;
CC KW Glycoprotein; Phosphorylation; Sialic acid; Signal.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 294 Osteopontin.
FT SITE 144 146 Cell attachment site.
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT CONFLICT 43 43 L -> P (in Ref. 4).
FT CONFLICT 99 99 E -> G (in Ref. 3).
FT CONFLICT 122 122 V -> F (in Ref. 2).
SQ SEQUENCE 294 AA; 32459 MW; 9D5F32D67ABC53EA CRC64;

Query Match 33.9%; Score 113; DB 1; Length 294;
Best Local Similarity 62.5%; Pred. No. 0.0022;
Matches 20; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 7 EVFTPVVTVTDYDGRGDSVYGRKSKKFR 38
: |||:||||| :||||| :||||| :
Db 129 DTFPTPIPTVDVNGRGLSLAYGLRSKRSFQ 160

RESULT 12
Q6N617 PRELIMINARY; PRT; 165 AA.
AC Q6N617;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Collagen triple helix repeat precursor.
GN OrderedLocusNames=RPA2801;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RA "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris";
RL Nat. Biotechnol. 22:55-61(2004).
RL EMBL; BX572602; CAE28243.1; -;
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
KW Collagen; Complete proteome; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 165 AA; 15559 MW; 92F507AE948A0F67 CRC64;

Query Match 33.3%; Score 111; DB 2; Length 165;
Best Local Similarity 91.7%; Pred. No. 0.002;
Matches 22; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 41 AGAAG--GPAGPAGPAGPAGPAGP 62
||||| ||||||| |||||||
Db 104 AGAAGPAGPAGPAGPAGPAGPAGP 127

RESULT 13
OSTP RAT
ID OSTP RAT STANDARD; PRT; 317 AA.
AC P08721;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Osteopontin precursor (Bone sialoprotein I) (Secreted phosphoprotein
DE 1) (SPP-1).
GN Name=Spp1; Synonyms=2b7, Spp-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93054745; PubMed=1429723;
RX Singh K., Mukherjee A.B., de Vouge M.W., Mukherjee B.B.;
RA "Differential processing of osteopontin transcripts in rat kidney-and
RT osteoblast-derived cell lines";
RL J. Biol. Chem. 267:23847-23851(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87067405; PubMed=3024151;
RA Oldberg A., Franzen A., Heinegaard D.;
RA "Cloning and sequence analysis of rat bone sialoprotein (osteopontin)
RT cDNA reveals an Arg-Gly-Asp cell-binding sequence";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8819-8823(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Smooth muscle;
RX MEDLINE=94013467; PubMed=8408622;
RA Giachelli C.M., Bae N., Almeida M., Denhardt D.T., Alpers C.E.,
RA Schwartz S.M.;
RT "Osteopontin is elevated during neointima formation in rat arteries

RT and is a novel component of human atherosclerotic plaques.";
 RL J. Clin. Invest. 92:1686-1696(1993).
 CC -1- FUNCTION: Binds tightly to hydroxyapatite. Appears to form an
 CC integral part of the mineralized matrix. Probably important to
 CC cell-matrix interaction.
 CC -1- FUNCTION: Acts as a cytokine involved in enhancing production of
 CC interferon-gamma and interleukin-12 and reducing production of
 CC interleukin-10 and is essential in the pathway that leads to type
 CC I immunity (By similarity).
 CC -1- SUBUNIT: Ligand for integrin alpha-V/beta-3.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Extensively phosphorylated on serine residues.
 CC -1- PTM: N- and O-glycosylated.
 CC -1- SIMILARITY: Belongs to the osteopontin family.
 CC -----
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 CC -----
 CC EMBL; M99252; AAA41765.1; -;
 CC EMBL; M14656; AAA41762.1; -;
 CC PIR; A25917; A25917.
 CC RGD; 3752; Spp1.
 CC GO; GO:0005578; C:extracellular matrix; ISS.
 CC GO; GO:0005125; P:cytokine activity; ISS.
 CC GO; GO:0008083; P:growth factor activity; ISS.
 CC GO; GO:0005178; P:integrin binding; ISS.
 CC GO; GO:0006916; P:anti-apoptosis; ISS.
 CC GO; GO:0007267; P:cell-cell signaling; ISS.
 CC GO; GO:0007160; P:cell-matrix adhesion; ISS.
 CC GO; GO:0030595; P:immune cell chemotaxis; ISS.
 CC GO; GO:0050930; P:induction of positive chemotaxis; ISS.
 CC GO; GO:0030502; P:negative regulation of bone mineralization; ISS.
 CC GO; GO:0042102; P:positive regulation of T-cell proliferation; ISS.
 CC GO; GO:0045637; P:regulation of myeloid blood cell differenti. . .; ISS.
 CC GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 CC InterPro; IPR02038; Osteopontin.
 CC Pfam; PF00865; Osteopontin; 1.
 CC PRINTS; PR00216; OSTEOPONTIN.
 CC PROSITE; PS00884; OSTEOPONTIN; 1.
 CC Biomineralization; Cell adhesion; Cytokine; Glycoprotein;
 CC Phosphorylation; Sialic acid; Signal.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 317 Osteopontin.
 FT DOMAIN 86 96 Poly-Asp.
 FT SITE 144 146 Cell attachment site.
 FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 8 8 F -> L (in Ref. 2).
 SQ SEQUENCE 317 AA; 34963 MW; 73C85C21FF6F62310 CRC64;
 Query Match 33.3%; Score 111; DB 1; Length 317;
 Best Local Similarity 64.5%; Pred. No. 0.0038;
 Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 YQ 7 EVFTPVVPTVDYDGRGDSVVYGRSKSKKF 37
 DB 129 DVLTPITPTVDVDPGRGDSLAYGLRSKRSF 159
 RESULT 14
 ID P97827 PRELIMINARY; PRT; 317 AA.
 AC P97827;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Osteopontin.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=101116;
 RX [1] SEQUENCE FROM N.A.
 RC STRAIN=Wister;
 RA YAMAMOTO S., UEMURA T.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wister;
 RA Yamamoto S.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB001382; BAA19247.1; -;
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR GO; GO:0001503; P:ossification; IEA.
 DR InterPro; IPR002038; Osteopontin.
 DR Pfam; PF00865; Osteopontin; 1.
 DR PRINTS; PR00216; OSTEOPONTIN.
 DR SMART; SM00017; OSTEO; 1.
 DR PROSITE; PS00884; OSTEOPONTIN; 1.
 SQ SEQUENCE 317 AA; 34963 MW; 779A5F00F8862310 CRC64;
 Query Match 33.3%; Score 111; DB 2; Length 317;
 Best Local Similarity 64.5%; Pred. No. 0.0038;
 Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 YQ 7 EVFTPVVPTVDYDGRGDSVVYGRSKSKKF 37
 DB 129 DVLTPITPTVDVDPGRGDSLAYGLRSKRSF 159
 RESULT 15
 ID Q6XLZ9 PRELIMINARY; PRT; 200 AA.
 AC Q6XLZ9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DT Firtv-1-B37 precursor.
 OS Feldmannia irregularis virus a.
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
 RN NCBI_TaxID=231992;
 RX [1] SEQUENCE FROM N.A.
 RC STRAIN=Firtv-1;
 RX PubMed=14745530; DOI=10.1007/s00239-003-2501-Y;
 RA Delaroque N., Boland W., Muller D.G., Knippers R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY225134; AAR26912.1; -;
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0008817; P:phosphate transport; IEA.
 DR InterPro; IPR008160; Collagen.
 DR Pfam; PF01391; Collagen; 2.
 KW Signal.
 FT SIGNAL 1 26 Potential.
 SQ SEQUENCE 200 AA; 19104 MW; 1A35AB97C69244A2 CRC64;
 Query Match 32.4%; Score 108; DB 2; Length 200;
 Best Local Similarity 80.8%; Pred. No. 0.0047;
 Matches 21; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
 YQ 40 PAGAGAG--GPAGPAGPAGPAGPAGPA 63
 DB 126 PKGPAGPVGVPAGPAGPAGPAGPA 151

Search completed: July 27, 2005, 18:14:51
Job time : 173 secs
